

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2002, 07:27:16 ; Search time 64.9 Seconds

(without alignments)
216.018 Million cell updates/sec

Title: US-09-854-731-4

Perfect score: 3260
Sequence: 1 MGOCYKGASGRTADDEGV.....LGFTRFLHGVTRGSTRRH 623

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents-AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3260	100.0	623	US-09-347-801-4	Sequence 4, Appl
2	2862	87.8	625	US-09-347-801-18	Sequence 18, Appl
3	1816.5	55.7	576	US-09-347-801-19	Sequence 19, Appl
4	883.5	27.1	639	US-09-347-801-17	Sequence 17, Appl
5	854	26.2	464	US-07-951-715A-22	Sequence 22, Appl
6	854	26.2	464	US-08-459-448A-22	Sequence 22, Appl
7	854	26.2	464	US-08-459-504B-22	Sequence 22, Appl
8	854	26.2	464	US-08-459-504B-22	Sequence 22, Appl
9	854	26.2	464	US-08-459-504B-22	Sequence 22, Appl
10	854	26.2	464	US-08-459-504B-22	Sequence 22, Appl
11	817	25.1	463	US-07-951-715A-25	Sequence 25, Appl
12	817	25.1	463	US-08-459-504B-25	Sequence 25, Appl
13	817	25.1	463	US-08-459-504B-25	Sequence 25, Appl
14	817	25.1	463	US-08-459-504B-25	Sequence 25, Appl
15	817	25.1	463	US-08-459-504B-25	Sequence 25, Appl
16	742	22.8	408	US-07-951-715A-21	Sequence 21, Appl
17	742	22.8	408	US-08-459-448A-21	Sequence 21, Appl
18	742	22.8	408	US-08-459-504B-21	Sequence 21, Appl
19	742	22.8	408	US-08-459-504B-21	Sequence 21, Appl
20	742	22.8	408	US-08-459-504B-21	Sequence 21, Appl
21	548	16.8	456	US-08-464-164-2	Sequence 2, Appl
22	548	16.8	456	US-08-338-057-2	Sequence 2, Appl
23	505.5	15.5	370	US-08-668-416-2	Sequence 2, Appl
24	505.5	15.5	370	US-08-878-989-19	Sequence 19, Appl
25	497	15.2	448	US-09-272-796-19	Sequence 19, Appl
26	497	15.2	448	US-09-159-385-2	Sequence 2, Appl
27	496.5	15.2	454	US-09-186-777-2	Sequence 2, Appl
				US-09-159-385-1	Sequence 1, Appl

28	496.5	15.2	454	US-09-186-277-1	Sequence 1, Appl
29	486.5	14.9	424	US-08-715-568A-1	Sequence 1, Appl
30	482.5	14.8	343	US-08-878-989-5	Sequence 5, Appl
31	482.5	14.8	343	US-09-272-796-5	Sequence 5, Appl
32	472	14.5	111	US-09-347-801-8	Sequence 8, Appl
33	465	14.3	264	US-07-857-224B-24	Sequence 24, Appl
34	457	14.0	157	US-09-347-801-6	Sequence 6, Appl
35	453	13.9	1423	US-08-810-712-10	Sequence 10, Appl
36	450	13.8	264	US-07-857-224B-18	Sequence 18, Appl
37	449	13.8	331	US-08-810-712-24	Sequence 24, Appl
38	444.5	13.6	387	US-08-713-828-3	Sequence 3, Appl
39	444.5	13.6	387	US-08-919-627-3	Sequence 3, Appl
40	444.5	13.6	387	US-09-096-245-3	Sequence 3, Appl
41	444	13.6	264	US-07-857-224B-19	Sequence 19, Appl
42	434.5	13.3	388	US-08-713-828-5	Sequence 5, Appl
43	434.5	13.3	388	US-08-919-627-5	Sequence 5, Appl
44	434.5	13.3	388	US-09-096-245-5	Sequence 5, Appl
45	421.5	12.9	388	US-08-713-828-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-09-347-801-4
; Sequence 4, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen Steve
; APPLICANT: Lee, Jian Ming
; FILE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-347-801-4

Query Match	Score	DB 4	Length	623
Best Local Similarity	100.0%	Pred. No. 3.8e-254		
Matches 623; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	MGOCYKGASGRTADDEGVYTERHQSPPPANGLPSTPRQQAQAQAQVCTPRRRGSKSG	60		
DB 1	MGOCYKGASGRTADDEGVYTERHQSPPPANGLPSTPRQQAQAQAQVCTPRRRGSKSG	60		
QY 61	STFGHQTPVAMPSPYPSGASPLPACVSPSPARSTPRRFFKRPFPSPAKHAKATLA	120		
DB 61	STFGHQTPVAMPSPYPSGASPLPACVSPSPARSTPRRFFKRPFPSPAKHAKATLA	120		
QY 121	KRLGGKKEETIPEEGVGAGGGGAADAEFERPLDKTFGFSKNGAYELKEVGR	180		
DB 121	KRLGGKKEETIPEEGVGAGGGGAADAEFERPLDKTFGFSKNGAYELKEVGR	180		
QY 181	GHFQTCGSAVVKKGKGYKQTAIVAKKMTTASIEDVREVKILRALSGHNNLVKFEY	240		
DB 181	GHFQTCGSAVVKKGKGYKQTAIVAKKMTTASIEDVREVKILRALSGHNNLVKFEY	240		
QY 241	DACEDGLNVIYVMECEGELLDRILANGRTEDDAIAIYVQIISVAFCHLQGVHRD	300		
DB 241	DACEDGLNVIYVMECEGELLDRILANGRTEDDAIAIYVQIISVAFCHLQGVHRD	300		
QY 301	LKPENFLFTTDENAPMLIDFGLSDFTRPDERLNDIGSAYVVAPEVLHRSYSMEADIW	360		
DB 301	LKPENFLFTTDENAPMLIDFGLSDFTRPDERLNDIGSAYVVAPEVLHRSYSMEADIW	360		

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QY 361 SIGVITVILGSRPFMAWTEGIFRSVLRADPNFDDSPMTVSAEKDFVKRLNDYR 420
DB 361 SIGVITVILGSRPFMAWTEGIFRSVLRADPNFDDSPMTVSAEKDFVKRLNDYR 420
QY 421 KRMVAVQALHPWLRDEQROIPDLILFRILKOYLATPLKRLALKALSKALREDELLYL 480
DB 421 KRMVAVQALHPWLRDEQROIPDLILFRILKOYLATPLKRLALKALSKALREDELLYL 480
QY 481 KLOFKLEPRDGFVSLDNFRATLRYLTDAKESRVLEFHLAELPLAYRMDEEECAAA 540
DB 481 KLOFKLEPRDGFVSLDNFRATLRYLTDAKESRVLEFHLAELPLAYRMDEEECAAA 540
QY 541 ISPVQLEALERWEIAGTAFOQFEQGNRYISVEELAOELNAPTHYSIVQWIRKSDG 600
DB 541 ISPVQLEALERWEIAGTAFOQFEQGNRYISVEELAOELNAPTHYSIVQWIRKSDG 600
QY 601 LNFLGFTKFLHGVITGINSNRRH 623
DB 601 LNFLGFTKFLHGVITGINSNRRH 623
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RESULT 2
US-09-347-801-18
; Sequence 18, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 18
; LENGTH: 625
; TYPE: PRT
; ORGANISM: Zea mays
US-09-347-801-18
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Query Match 87.8%; Score 2862; DB 4; Length 625;
Best Local Similarity 87.7%; Pred. No. 3, 9e-222;
Matches 561; Conservative 16; Mismatches 31; Indels 32; Gaps 7;
QY 1 MGOCYGR--GASGRT---ADDEGVTEHOSPPRANGLPSTPRQQAQAQOVGTGPRRR 55
DB 1 MGOCYGRAGASRSHADADPSGAGSVAPSPPLRANGAPLP-----ATPRRH 47
QY 56 GSKSGSTTPGHQ---TPG--VAMPSPYSGASPLPAGVSPSPARSTRFRFRPPPS 110
DB 48 --KSGSTTPVHNHQAATPAAWSPYRAGASPLPAGVSPSPARSTRFRFRPPPS 105
QY 111 PAKHIKATLAKKLGCGKPKGCTPREBGVAGAGGGG-----GAADGAETTERLDKTCG 163
DB 106 PAKHIKATLAKKLGCGKPKGCTPREBGVAGAGAGAGAGAAVGAADSDADRLDKTCG 165
QY 164 FSNFNGAKYELGKVGNGHGTCSAVVKKGEYKQTVAVKIIAKKMTAISIEDVRE 223
DB 166 FAKNFGAKYDLGKVGNGHGTCSAVVKKGEYKQTVAVKIIAKKMTAISIEDVRE 225
QY 224 VKILRLSGHNNLVKFTYDACEGLNLYIWMELCEGELLDRILARGRYTEEDAKAIYVQ 283
DB 226 VKILRLSGHNNLVKFTYDACEGLNLYIWMELCEGELLDRILARGRYTEEDAKAIYVQ 285
QY 284 ILVAVFCHLQGVVHRDLKPENFLFTTRDENAPKLIIDFGLSDFTRPDERLNDIVGAYY 343
DB 286 ILVAVFCHLQGVVHRDLKPENFLFTTRDENAPKLIIDFGLSDFTRPDERLNDIVGAYY 345
QY 344 VAEVVLHRSYSMEADTWSIGVITVILGSRPFMAWTEGIFRSVLRADPNFDDSPMTV 403
DB 344 VAEVVLHRSYSMEADTWSIGVITVILGSRPFMAWTEGIFRSVLRADPNFDDSPMTV 403
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DB 346 VAEVVLHRSYSMEADTWSIGVITVILGSRPFMAWTEGIFRSVLRADPNFDDSPMSV 405
QY 404 SAAKDFVVRFLNKDQYRKMTAVQALTHPWLDEQROIPDLILFRILKOYLATPLKRL 463
DB 406 SAAKDFVVRFLNKDQYRKMTAVQALTHPWLDEQROIPDLILFRILKOYLATPLKRL 465
QY 464 ALKALSKALREDELLYLKLOFKLEPRDGFVSLDNFRATLRYLTDAKESRVLEFHLA 523
DB 466 ALKALSKALREDELLYLKLOFKLEPRDGFVSLDNFRATLRYLTDAKESRVLEFHLA 525
QY 524 EPLAYRNDDEEECAAISPVQLEALERWEIAGTAFOQFEQGNRYISVEELAOELNLA 583
DB 526 EPLAYRNDDEEECAAISPVQLEALERWEIAGTAFOQFEQGNRYISVEELAOELNLA 585
QY 584 PTHYSIVQWIRKSDGKLNFLGFTKFLHGVITGINSNRRH 623
DB 586 PTHYSIVQWIRKSDGKLNFLGFTKFLHGVITGINSNRRH 625
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RESULT 3
US-09-347-801-19
; Sequence 19, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 19
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-347-801-19
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Query Match 55.7%; Score 1816.5; DB 4; Length 576;
Best Local Similarity 57.3%; Pred. No. 4, 3e-138;
Matches 358; Conservative 95; Mismatches 109; Indels 63; Gaps 9;
QY 1 MGOCYGRAGASGRADDEGVTEHOSPPRANGLPSTPRQQAQAQOVGTGPRRRGSKSG 60
DB 1 MGICGK-----PVEOOS---KSLPVSGETNEAPNSQ----- 30
QY 61 STTPGHQTPGVAMPSPYSGASPLPAGVSPSPA-----RSTRFRFRFRPPPSPAKHI 115
DB 31 ---PRAKSGGFYSP-----SPVPSLPKSSPSVSSVSTPLRFRFRPPPSPAKHI 81
QY 116 KATLAKRLGCGKPKGCTPREBGVAGAGGGGGAADGATERPLDKTCGSKNFGAKYELG 175
DB 82 RAFLARRGVVAPNVSYSIPE-----GKCEIGLDKSKGFSQAFSHIED 126
QY 176 KEVGRGHGHTCSAVVKKGEYKQTVAVKIIAKKMTAISIEDVRRVQKILRLSGHNN 235
DB 127 GEVGRGHGHTCSAKGKGSIGKQEVAKVLPKSMNTAILEVSRVKKLRLALTGHN 186
QY 236 LVKFTDACEGLNLYIWMELCEGELLDRILARGRYTEEDAKAIYVQILSVAVFCHLQ 295
DB 187 LVQFYDAFEDDENYIWMELCKGELLDRILARGRYTEEDAKAIYVQILSVAVFCHLQ 246
QY 296 VVHRDLKPENFLFTTRDENAPKLIIDFGLSDFTRPDERLNDIVGAYYVAEVLHRSYSM 355
DB 247 VVHRDLKPENFLFTKQETSPKLIIDFGLSDYVPRDLNDIVGAYYVAEVLHRTYGT 306
QY 356 EADTWSIGVITVILGSRPFMAWTEGIFRSVLRADPNFDDSPMTVSAEKDFVKRL 415
DB 307 EADTWSIGVITVILGSRPFMAWTEGIFRSVLRADPNFDDSPMTVSAEKDFVKRL 366
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[illegible]

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RESULT 4
US-09-347-801-17
Sequence 17, Application US/09347801
Patent No. 6262345
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jan Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: B8-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGTH: 639
TYPE: PRT
ORGANISM: Zea mays
US-09-347-801-17

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Query Match	27.1%;	Score 883.5;	DB 4;	Length 639;
Best Local Similarity	35.4%;	Pred. No. 5.4e-63;		
Matches 219;	Conservative 102;	Mismatches 234;	Indels 63;	Gaps 17

QY	25	OSPPRANLEPSTRPQQAQAQAQVSTRPRRGRSGSGSTTGHGQHPGVAMSPYRPSGASP	84
Db	25	KTPOEGDLR-----AAANGPBGAGAGSOSALPKRASDVHNHVAVOS-----EAP	69
QY	85	LPAGVSPSPARSTRPRRFKKRPFRPPSPAKNIK-ATLAKRLIGG-----KPECTIPEEG	137
Db	70	EPVKITAAHSEPRALVANSSEAPRYKITAHSHERPARMAKPEGAANAANSPSPSPRRQYK	129
QY	138	GVGAGGGGGGAADAETERPDLKTFGFSKMFCAKYELEKEVGRGHG--HTCSAVVXKE	195
Db	130	RVSASGILLGSVLRKTE-----NLKDXYSIGRLRGQGFCTHLC---VERA-174	
QY	196	YKGQVAVAKITAKAKMTAISEVYRREVKTLRLSGHNILVYKYDCEGSLVNYIYEL	255
Db	175	-TGKELAKSLIKRLGDDDEVEVERREIQIHMHLASHSPVAGIRGAYEDAVAAVHIMEL	233
QY	256	CGEGELDRITLARGRYEEDAKALVQILISVAFCHLGQVNHDKLPENFLTTRRENA	315
Db	234	CGGGELFRIRYR-GHTYERRAAELARYIVGVNACHSMSGMHNDKLPENLFEADHSEA	292
QY	316	PMKLDFELISFIRPDERLNDIVSAYVAVPEVLRHSYSMEADIMSIGVITYILCSRP	375
Db	293	ALKTIDELSTFFRRGOLFPTDVVSSPYTVAEYELKRRGRPADVMSAGVIITYILCGVP	352
QY	376	FWARTESGIFRSVLRADENFDSPPTVASAEAKDFVARKFLNKDYRKRTMAVOALTFRWLR	435
Db	353	FMAENEGQIFEEVILHGRIDFESSEPMISDQAKDLVRMLVROBRKRLTAHEVLRHPMV-	411
QY	436	DEGRQI-----PDILIFRLIQYLRATPLKALKALSKALREDEBLTYLKIQGFLE	488

[illegible]

RESULT 5
US-07-951-715A-22
; Sequence 22, Application US/07951715A
; Data was received

APPLICANT: Koziet, Michael G.
 APPLICANT: Desai, Nalin M.
 APPLICANT: Lewis, Kelly S.
 APPLICANT: Kramer, Vance C.
 APPLICANT: Warren, Gregory W.
 APPLICANT: Evola, Stephen V.
 APPLICANT: Crossland, Lyle D.
 APPLICANT: Wright, Martha S.
 APPLICANT: Merlitt, Ellis J.
 APPLICANT: Launus, Karen L.
 APPLICANT: Rothstein, Steven J.
 APPLICANT: Bowman, Cindy G.
 APPLICANT: Dawson, John L.
 APPLICANT: Dunder, Erik M.
 APPLICANT: Pace, Gary M.
 APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 INSULINIC DNA ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30E
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/951,715A
FILING DATE: 25-SEP-1992
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spullin, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-16805/A/CGC 1577/CJH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEO ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO

FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /note- "derived protein sequence of
OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-07-951-715A-22

Query Match 26.2% Score 854; DB 1; Length 464;
Best Local Similarity 40.0%; Pred. No. 8.2e-61;
Matches 186; Conservative 88; Mismatches 163; Indels 28; Gaps 10;

156 RPLDTFGSKNFAGKELGKVGGRHFG--HTCSAVYKKGKGTAVYAKAKMTT 213
DB 4 RPE-----DVRATYSMGKELRGQGVTHLCT-----HRTSGELACKTIARKKLA 51
QY 214 AISEDVREVKILRALSGHNNLKYFYDACEGLNVIYVLCBGGELDRILARGRYT 273
DB 52 REDVDVREVOQMHLHSGQPNVGLRGAYEDKQSVHLMELCAGGELFDRITAR-GQYT 110
QY 274 EEDAKAIVVOILSVAFCHLQGVHRDLKPENFLETTDRDNAPKLIIDPGLSDPIRDER 333
DB 111 ERGAELRLAIYOIHTCHSMGVHRDIKPENFLLSKDDEAPLKAFTGLSVFKEGEL 170
QY 334 LNDIVGSAVYVAPVLRHSYMEADIMSGVITTYILLGSRPFWARTSGIFRSVLRADP 393
DB 171 LNDIVGSAVYVAPVLRHSYMEADIMSGVITTYILLGSRPFWARTSGIFRSVLRADP 393
QY 394 NEDDSPWPTVSAEAKDFKRLNKKRMTAVOALTHPMLRD--EQRIPLDILIRLI 451
DB 231 DLSEPPMHPISPGAKDLVKMKLINPKERLAFQVLNHPWKKEGDADPTPLDNLVLDRL 290
QY 452 KOYLRTPLKRLALKSKALREDELLYKLOFKLE-PRDGEVSLDNFRALTALRYLTDA 510
DB 291 KQFRAMNOFKKALRIIAGCLSEETITGLKEMFNIDKNSGTTIDELKHGLAKH-GPK 349
QY 511 MKESVLEFLHLEPLAVRRMDFEEFCAAIAPYOLELRMEELIAGTAFOQFDEGKRV 570
DB 350 LSDSEMEKLMKADADGNGLIDYDEFVATYV--HMKKLDL-EEHLTYATFOYFDKNSGY 405
QY 571 ISVEEL-----AOELNLAPHYSTVODMIRKSDGKLNFLCFTKFL 610
DB 406 ITRKELEHALKEOGLYDADKIKDITISDSDSDNGRIDYSEFVAMM 450

RESULT 6

US-08-459-448A-22
Sequence 22, Application US/08459448A
Patent No. 5859336

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalin M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Ewola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlino, Ellis J.
APPLICANT: Launus, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005

CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /note- "derived protein sequence of
OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-08-459-448A-22

Query Match 26.2% Score 854; DB 2; Length 464;
Best Local Similarity 40.0%; Pred. No. 8.2e-61;
Matches 186; Conservative 88; Mismatches 163; Indels 28; Gaps 10;

156 RPLDTFGSKNFAGKELGKVGGRHFG--HTCSAVYKKGKGTAVYAKAKMTT 213
DB 4 RPE-----DVRATYSMGKELRGQGVTHLCT-----HRTSGELACKTIARKKLA 51
QY 214 AISEDVREVKILRALSGHNNLKYFYDACEGLNVIYVLCBGGELDRILARGRYT 273
DB 52 REDVDVREVOQMHLHSGQPNVGLRGAYEDKQSVHLMELCAGGELFDRITAR-GQYT 110
QY 274 EEDAKAIVVOILSVAFCHLQGVHRDLKPENFLETTDRDNAPKLIIDPGLSDPIRDER 333
DB 111 ERGAELRLAIYOIHTCHSMGVHRDIKPENFLLSKDDEAPLKAFTGLSVFKEGEL 170
QY 334 LNDIVGSAVYVAPVLRHSYMEADIMSGVITTYILLGSRPFWARTSGIFRSVLRADP 393
DB 171 LNDIVGSAVYVAPVLRHSYMEADIMSGVITTYILLGSRPFWARTSGIFRSVLRADP 393
QY 394 NEDDSPWPTVSAEAKDFKRLNKKRMTAVOALTHPMLRD--EQRIPLDILIRLI 451
DB 231 DLSEPPMHPISPGAKDLVKMKLINPKERLAFQVLNHPWKKEGDADPTPLDNLVLDRL 290
QY 452 KOYLRTPLKRLALKSKALREDELLYKLOFKLE-PRDGEVSLDNFRALTALRYLTDA 510
DB 291 KQFRAMNOFKKALRIIAGCLSEETITGLKEMFNIDKNSGTTIDELKHGLAKH-GPK 349
QY 511 MKESVLEFLHLEPLAVRRMDFEEFCAAIAPYOLELRMEELIAGTAFOQFDEGKRV 570
DB 350 LSDSEMEKLMKADADGNGLIDYDEFVATYV--HMKKLDL-EEHLTYATFOYFDKNSGY 405


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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8587
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: protein
TOPOLOGY: linear
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION:
US-08-459-504B-22

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Query Match Best Local Similarity 26.28; Score 854; DB 3; Length 464; Pred. NO. 8.2e-61;

Matches 186; Conservative 88; Mismatches 163; Indels 28; Gaps 10;

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QY 156 RPLDKTFGSKNGKAYELKEVGRGHG--HTCSAVVKKGEYGVAVYKAKAMTT 213
DB 4 RPM-----DVRATYSMGKELRGQGVTHLCT-----HRTSGELACKTTAKRLAA 51
QY 214 AISEDVAREVKILRALSGHNNLVKFFDACEDEGLNVIYVMECEGELDRILARGGRY 273
DB 52 REDVDVAREVOIMHNSGQPNVVGAYGAYEDKOSVHLVMEACGELFPRIIAR-QGY 110
QY 274 EEDAKAIVQILSVVARCHGVVHNDLKRPENFLFTTRDENAMKILDEGLSPFIRDER 333
DB 111 ERGAELRLAIVQIVHTCHSMGVHNDIKPENFLLSKDEDAFLKATDFGLSVFREGEL 170
QY 334 LNDIVGSAVYVAREVLRHSYMEADIMSLGIVTYILLGSRPFWARTESGIFRSVLRAP 393
DB 171 LRDIVGSAVYVAREVLRKRYGPEADIMSVGMLYIFLAGVPPMAENKIFAILRGOL 230
QY 394 NFDSDPMPYSAKAKDFVRFKLDYRKRTAVQALTHPWLRD--DQROIPLDILFRLL 451
DB 231 DLSSEPMPLISPAKDLVKMLINPKERLTAFOVLNHPWIKEDGADPTPLDNNVLDRL 290
QY 452 KQYLRATPLKRLKALSKALREDELLYLQFKILE-PRDGVSLDNRRTALRLTLTA 510
DB 291 KQPRANNOFKKALRLITACLSSEETITGLKEMFNIDKNSGTTVLDLKHGLAKH-GPK 349
QY 511 MKRSRVLELHLALEPLAYRMDFEFCAAIISPYOLEALEREWEIAGTAFQOFDEGNRV 570
DB 350 LSSSEKELMEADADGNGLDIDYDEVFATV--HNNKIDR-EBHLVYTAFOYFDKNSGY 405
QY 571 ISVEEL-----AOELNLAFTHSYVQDMTRKSDKLNPLGFTKFL 610
DB 406 TKREELHALKRGGLYADKIDKIDISDSDNDGRIDYSEFVAM 450

```

RESULT 9
US-08-459-444-22

Sequence 0, Application US/08459444A
Patent No. 6121014

GENERAL INFORMATION:

APPLICANT: Koziet, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED

NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,444A

FILING DATE: 02-Jun-1995

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8587

INFORMATION FOR SEQ ID NO: /note- "derived protein sequence of

pollen specific CDPK as disclosed in Figure 34."

SEQUENCE CHARACTERISTICS:

LENGTH: 464 amino acids

TYPE: amino acid

STRANDEDNESS: single

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: Protein

LOCATION: 1..464

SEQUENCE DESCRIPTION: SEQ ID NO: 22:

US-08-459-444-22

Query Match Best Local Similarity 26.28; Score 854; DB 3; Length 464; Pred. NO. 8.2e-61;

Matches 186; Conservative 88; Mismatches 163; Indels 28; Gaps 10;

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QY 156 RPLDKTFGSKNGKAYELKEVGRGHG--HTCSAVVKKGEYGVAVYKAKAMTT 213
DB 4 RPM-----DVRATYSMGKELRGQGVTHLCT-----HRTSGELACKTTAKRLAA 51
QY 214 AISEDVAREVKILRALSGHNNLVKFFDACEDEGLNVIYVMECEGELDRILARGGRY 273

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us-09-854-731-4.rai

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1 APPLICANT: Rothstein, Steven J.
2 APPLICANT: Bowman, Cindy G.
3 APPLICANT: Dawson, John L.
4 APPLICANT: Dunder, Erik M.
5 APPLICANT: Pace, Gary M.
6 APPLICANT: Suttle, Janet L.
7 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
8 TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
9 NUMBER OF SEQUENCES: 94
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: No. 3659336art's Corporation
12 STREET: Patent 6 Triemark Dept., 520 White Plains
13 STREET: Rd., POB 2005
14 CITY: Tarrytown
15 STATE: New York
16 COUNTRY: USA
17 ZIP: 10591-9005
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: Floppy disk
20 COMPUTER: IBM PC compatible
21 OPERATING SYSTEM: PC-DOS/MS-DOS
22 SOFTWARE: PatentIn Release #1.0, Version #1.30
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/08/459,448A
25 FILING DATE: 02-JUN-1995
26 CLASSIFICATION: 800
27 PRIOR APPLICATION DATA:
28 APPLICATION NUMBER: US 07/951,715
29 FILING DATE: 25-SEP-1992
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: US 07/772,027
32 FILING DATE: 04-OCT-1991
33 ATTORNEY/AGENT INFORMATION:
34 NAME: Pace, Gary M.
35 REGISTRATION NUMBER: 40403
36 REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
37 TELECOMMUNICATION INFORMATION:
38 TELEPHONE: (919)541-8582
39 TELEFAX: (919)541-8689
40 INFORMATION FOR SEQ ID NO: 25:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 463 amino acids
43 TYPE: amino acid
44 STRANDEDNESS: single
45 TOPOLOGY: linear
46 MOLECULE TYPE: protein
47 HYPOTHEICAL: NO
48 FEATURE:
49 NAME/KEY: Protein
50 LOCATION: 1..463
51 OTHER INFORMATION: /note="protein sequence for
52 soybean CDPK as shown in Figure 34."
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	Query Match	25.1%	Score 817;	DB 2;	Length 463;
	Best Local Similarity	38.9%;	Pred. No. 7.7e-58;		
	Matches 178; Conservative	94;	Mismatches 160;	Indels	26; Gaps 11
OY	165 SKNGANGAYELGKEVGRGHFGHT--CSAVVKKEYGVQGVAVAKIITAKAKMTAISIEVVR	222			
Dd	6 TONIREYVEYGRLLGGCGFCTTPECTRRASGKF-----ACKSLPKRKLCKEDYEVDVMR	60			
OY	223 EVKILRLSGHNHLVVFYACDEGLINVIYMELCEGSELDRIILARGRYTEBDAAKAVI	282			
Dd	61 EIQLMHLISHNAVVRIEGTGEDSPVAHVLWMLCEGSELFPRIYQK-GHSSEQAARLKK	119			
OY	283 QLSVVAFCFLGCVLRDRLKENELFTTRDNAENAPMKLIDGLSDFIPDERLNDIVGSAY	342			
Dd	120 TLVEYVLEACHSLGVNHRDLKPENLFETIIDDAKATIDGLSFYFKPGESFCFDVGSPY	179			
OY	343 YVAPEVLHNSIKSMEDIISIGVTITLLCGSRPMATGESIFRSVLRADPNDDSDPWT	402			

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Db      180  YVAPEVLRKLYGESPVSAGVILYLLSGVPFPAESEPFRQIILGKLDFHSEBPWS 239
Qy      403  VSAEADPEVKRFLNKKDYRRKMTAVOALTHPMLRDEQ--RQIPDLILFRLIKOYLATPL 460
Db      240  IISDASDILIRKMLDQPKFRTLPAHEVLRHPMIVDNLAPDQPLDSAVLSLKQFSAMNKL 299
Qy      461  KRLLAKALKALREBDELLYKLOFVLLP-PDQGVSLDNFRTALTRYLTDAMKESRYLEF 519
Db      300  KKALAVIERLRSEEGGKELFKMIDTNSGTTTDELDKGLKRGSELM-ESEIKDL 358
Qy      520  LHALEPLAVRMDPEFCAAAISPYOLEALRMEELAGTAFOQPEOGNIVISVEPLAQ 578
Db      359  MDAADIDKSGTIDYGEFTAAVY---HLMKTERENLV-SAFSVFADKDGSGYITLDEIQQA 414
Qy      579  --ELNIAPHYISYVDWIRK----SDGLANTLGTRKL 610
Db      415  CKDQGLDDIH---IDDMTKELDQDNDQDIDGEPAAAM 449

RESULT 12
US-08-459-595A-25
; Sequence 25, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Kozziel, Michael G.
; APPLICANT: Desai, Nalin M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evoila, Stephen V.
; APPLICANT: Crossland, Lytle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttler, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; NUMBER OF INVENTIONS: 1
; INSECTICIDAL ACTIVITY IN MAIZE
; CORRESPONDENCE ADDRESS: 94
; ADDRESSEE: No. 6018104artlis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689

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Db 240 ISDSAKLIRKMDONKRTLTAEVL RHPVIYDNIAPDKPLDSAVLSRLKQFSAMNKL 299
QY 461 KRLAKLAKSALREDELLYLKLOFLE-PRDFVSLDNRTALTRYLTDAMKESRYLEF 519
Db 300 KKMALRYAERLSEELGKLEFKMIDTNSGTTTFDELKDLKRVGSELM-ESKIKDL 358
QY 520 LHALEPLAYRMDPEEFCAAIISPYOLEALERMEETAGTAFQOFEQGNRVISVEELAO- 578
Db 359 MDADIDKSGTIDYGEFIATV---HLNKLREBNLY-SAFSYFDKDGSGYITLDEIQQA 414
QY 579 --ELNLAPTHYSIVODIRK---SDGKLNFLGFTKFL 610
Db 415 CKDEGLDDIH---IDMWIKETIDQNDQIDYGEFAAM 449

RESULT 14
US-08-459-444-25
Sequence 0, Application US/08459444A
Patent No. 6121014

GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: /note- "protein sequence for
soybean CDPK as shown in Figure 34."

SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-459-444-25

Query Match 25.1%; Score 817; DB 3; Length 463;
Best Local Similarity 38.9%; Pred. No. 7.7e-58;
Matches 178; Conservative 94; Mismatches 160; Indels 26; Gaps 11;

QY 165 SNNFAGKYLKGVGRGHGHT--CSAVVKKGEKQGVAVKAIKAKMTAISIEDVR 222
Db 6 TONIREVEYEVGRKLGQGGFTTPECTRASGK-----ACKSLPKRLCKEYEDVWR 60
QY 223 EYKILRASNNLVKFTDACEDELANYIVVLECEGELDRILAKGRTYEDAKAIV 282
Db 61 EIQIHLSEHANVVRLEGTYEDSTAVHLVMELEGELEFDRYOK-GHYSEKQAARLK 119
QY 283 QILSVAFCHQGVNHRDLKPFNFLETTSDENAPMKLIDGSLDFIRPDELDNIYGSAY 342
Db 120 TIVEVVEACHSLGVNHRDLKPFNFLETTSDENAPMKLIDGSLDFIRPDELDNIYGSAY 342
QY 343 YVAPVLRHRSYMDADISGIVTYILLCSRPWARTESGIFRSYLRADPNFDSFMP 402
Db 180 YVAPVLRHRSYMDADISGIVTYILLCSRPWARTESGIFRSYLRADPNFDSFMP 402
QY 403 VSAAKDFVKKRFLNKQYRKMTAVQALTHPLRDEQ--RQIPDLIFRLIKOYLATPL 460
Db 240 ISDSAKLIRKMDONKRTLTAEVL RHPVIYDNIAPDKPLDSAVLSRLKQFSAMNKL 299
QY 461 KRLAKLAKSALREDELLYLKLOFLE-PRDFVSLDNRTALTRYLTDAMKESRYLEF 519
Db 300 KKMALRYAERLSEELGKLEFKMIDTNSGTTTFDELKDLKRVGSELM-ESKIKDL 358
QY 520 LHALEPLAYRMDPEEFCAAIISPYOLEALERMEETAGTAFQOFEQGNRVISVEELAO- 578
Db 359 MDADIDKSGTIDYGEFIATV---HLNKLREBNLY-SAFSYFDKDGSGYITLDEIQQA 414
QY 579 --ELNLAPTHYSIVODIRK---SDGKLNFLGFTKFL 610
Db 415 CKDEGLDDIH---IDMWIKETIDQNDQIDYGEFAAM 449

RESULT 15
US-07-951-715A-21
Sequence 21, Application US/07951715A
Patent No. 5625136

GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.
Rothstein, Steven J.
Applicant: Bowman, Cindy G.
Applicant: Dawson, John L.
Applicant: Dunder, Erik M.
Applicant: Pace, Gary M.
Applicant: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: USA
ZIP: 10532

COMPUTER READABLE FORM:

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2002, 06:25:16 ; Search time 71.49 Seconds

(Without alignments)
663.824 Million cell updates/sec

Title: US-09-854-731-4

Perfect score: 3260

Sequence: 1 MGOCYGGKSGRTADDEGV.....LGFTKFLHGVIRGSRTRH 623

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: pirl:*\n2: pirl:*\n3: pirl:*\n4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2862	87.8	625	2 T02033	calcium/calmodulin
2	2831	86.8	607	2 T03023	calcium-dependent
3	2179	66.8	595	2 B84906	probable calcium-d
4	1970	60.4	594	2 T43842	calcium dependent
5	1917	58.8	601	2 T46084	CDPK-related prote
6	1894	58.1	602	2 S60052	calcium-dependent
7	1829	56.1	577	2 T51264	calcium-dependent
8	1816.5	55.7	606	2 T02105	calcium-dependent
9	1760.5	54.0	576	2 D96532	probable CDPK-rela
10	1153.5	35.4	571	2 T00835	calcium-dependent
11	1080	33.1	536	2 T05500	calcium-dependent
12	923.5	28.3	583	2 H84810	probable calcium-d
13	904.5	27.7	533	2 S56552	calcium-dependent
14	903.5	27.7	529	1 S71774	calcium-dependent
15	895.5	27.5	573	2 T09940	calcium-dependent
16	889.5	27.3	540	1 T01889	calcium-dependent
17	886	27.2	531	1 T02993	calcium-dependent
18	886	27.2	534	1 T02784	calcium-dependent
19	883.5	27.1	639	1 T05476	calcium-dependent
20	877	26.9	610	1 A49082	calcium-dependent
21	865	26.5	513	1 T02259	calcium-dependent
22	860	26.4	554	1 T03263	calcium-dependent
23	859.5	26.4	531	2 D85059	probable calcium d
24	854	26.2	490	1 S71776	calcium-dependent
25	853.5	26.2	465	1 T03024	calcium-dependent
26	852.5	26.2	465	1 T46189	calcium-dependent
27	848.5	26.0	553	2 T02139	calcium-dependent
28	847.5	26.0	532	2 T14335	protein kinase, ca
29	843.5	25.9	492	1 T03271	calcium-dependent

30	843.5	25.9	514	2 T10938	calcium-dependent
31	841.5	25.8	521	2 G96543	calcium-dependent
32	838	25.7	493	1 S46283	calcium-dependent
33	837.5	25.7	541	2 F96776	hypothetical prote
34	835	25.6	545	2 H86322	calcium-dependent
35	834	25.6	503	2 T51156	calcium-dependent
36	832	25.5	538	2 T08874	calcium-dependent
37	829	25.4	495	1 S46284	calcium-dependent
38	828.5	25.4	533	1 S71778	calcium-dependent
39	824.5	25.3	501	2 G85097	hypothetical prote
40	821	25.2	520	2 F85059	probable calcium d
41	820.5	25.2	582	2 E84721	probable calcium d
42	819.5	25.1	487	1 S71770	calcium-dependent
43	817	25.1	508	1 A43713	calcium-dependent
44	816.5	25.0	556	2 T06126	calcium-dependent
45	811	24.9	544	2 D84550	probable calmodulin

ALIGNMENTS

RESULT 1

T02033
calcium/calmodulin-dependent protein kinase homolog - maize

C:Species: Zea mays (maize)

C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 17-Nov-2000

C:Accession: T02033; T02994; T01694

R:Lu, Y.T.; Hidaka, H.; Feldman, L.J.

Planta 199, 18-24, 1996

A:Title: Characterization of a calcium/calmodulin-dependent protein kinase homolog fr

A:Reference number: Z14504; MUID:96236830

A:Accession: T02033

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-625 <LUY>

A:Cross-references: EMBL:S82324; NID:g1839596; PIDN:AA847181.1; PID:g1839597

A:Experimental source: CV, Merit

R:Furumoto, T.; Ogawa, N.; Hata, S.; Izui, K.

FEBS Lett. 396, 147-151, 1996

A:Title: Plant calcium-dependent protein kinase-related kinases (CKR) do not require

A:Reference number: Z14398; MUID:97072168

A:Accession: T02994

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 29-146, 'GA', 147-625 <FUR>

A:Cross-references: EMBL:D84507; NID:g1313906; PIDN:BA12691.1; PID:g1313907

A:Experimental source: strain inbred line H84; root

A:Accession: T01694

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 174-398, 'G', 400-625 <FUR>

A:Cross-references: EMBL:D8485; NID:g2443387; PIDN:BA22410.1; PID:g2443388

A:Experimental source: leaf

C:Genetics:

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

F:172-436/Domain: protein kinase homology <KIN>

A:Title: BAA12691.1

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

F:172-436/Domain: protein kinase homology <KIN>

A:Title: BAA12691.1

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

F:172-436/Domain: protein kinase homology <KIN>

A:Title: BAA12691.1

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

F:172-436/Domain: protein kinase homology <KIN>

A:Title: BAA12691.1

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

F:172-436/Domain: protein kinase homology <KIN>

A:Title: BAA12691.1

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

F:172-436/Domain: protein kinase homology <KIN>

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Db 106 PAHKIKATLAKRLGGCKREKGTIPBEGGACAGAGAGAAVGAADSAEDRPDLKTTG 165
Oy 164 ESKNEGKAYELGKVEVGGHGHGHCASAVVKKGEYKGTVAVKTIKAKMTAISIEDVRE 223
Db 166 FAKFPGAKYDLGKEVGGHGHGHCASAVVKKGEHKGHTVAVKIISKAKMTAISIEDVRE 225
Oy 224 VKTLRALSGHNNVVKFEADCEGLNLYIYMECEGELLDRILARGRYTEEDAKAIYVQ 283
Db 226 VKTLKALSGHNNVVKFEADCEGLNLYIYMECEGELLDRILARGRYTEEDAKAIYVQ 285
Oy 284 ILSVAFCHLQGVVHDLKPENFLFTTRDENAPMKLIDGLSDPIRPERLNDIVGSAY 343
Db 286 ILSVAFCHLQGVVHDLKPENFLFTTRDENAPMKLIDGLSDPIRPERLNDIVGSAY 345
Oy 344 VAEVLRHSYSMEADIMSGVITYILGSRPFWARTESGIFRSYLRADPNFDDSPWPSV 403
Db 346 VAEVLRHSYSMEADIMSGVITYILGSRPFWARTESGIFRSYLRADPNFDDSPWPSV 405
Oy 404 SAKAKPFVKRFELNKDYRKMTAVOALTHPMLRDEORQIPDLILFRILKQYLRAATPLKRL 463
Db 406 SAKAKPFVKRFELNKDYRKMTAVOALTHPMLRDEORQIPDLILFRILKQYLRAATPLKRL 465
Oy 464 ALKALSKALREDELTYLKQFLKLEPRROGFSVLDNFRALTTRYLDAMKESVLEFLHAL 523
Db 466 ALKALSKALSEDEBLTYLKQFLKLEPRROGFSVLDNFRALTTRYLDAMKESVLEFLHAL 525
Oy 524 EPLAVRRMDEEFCAALSPYOLEALEREWEIAGTAFQOEEOGNRVISVEELAOELNLA 583
Db 526 EPLAVRRMDEEFCAALSPYOLEALEREWEIAGTAFQOEEOGNRVISVEELAOELNLA 585
Oy 584 PTHYSIVQDMIRKSGKLNFLGFTKFLHGVTIRGSNTRRH 623
Db 586 PTHYSIVQDMIRKSGKLNFLGFTKFLHGVTIRGSNTRRH 625

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RESULT 2
703023
calcium-dependent protein kinase-related protein kinase - maize
C:Species: Zea mays (maize)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T03023
R:Furumoto, T.; Ogawa, N.; Hata, S.; Izui, K.
FEBS Lett. 396, 147-151, 1996
A:Title: Plant calcium-dependent protein kinase-related kinases (CRK) do not require cal
A:Reference number: Z14398; MUID:97072168
A:Accession: T03023
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-607 <FUR>
A:Cross-references: EMBL:DB4508; NID:g1313908; PIDN:BAAL2692.1; PID:g1313909
A:Experimental source: strain inbred line H84; root
A:Note: does not require calcium for its activity
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
F:154-418/Domain: protein kinase homology <KIN>

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Query Match 86.8%; Score 2831; DB 2; Length 607;
Best Local Similarity 88.3%; Pred. No. 1.1e-100;
Matches 553; Conservative 18; Mismatches 33; Indels 22; Gaps 7;
Oy 1 MGOCYGRK-GASGRADDEGGVTEHQSPPPANGLPSTPRQQAQAQAQVGTPRRRGSK 58
Db 1 MGOCYGRKAGASRRADHDVAAP--PSLPANGAP--TPQQA-----TPGR--K 47
Oy 59 SGSTTP-GHQTGVAMPSPYPSGASPLPAGVSPSPARSTPRFRFRPPPPPAKHAKA 117
Db 48 SGSTTPVNHQAATTPSPYRAGASPLPAGVSPSPARSTPRFRFRPPPPPAKHAKA 107
Oy 118 TLAKRLGGCKREKGTIPBEGGACAGAGGAGADGAETPRDLKTTGFSKNGAKYELGKE 177
Db 108 TLAKRLGGCKREKGTIPBEGGACV-----AADSAEABRPDLKTTGFAANNFGAKYDLGKE 161

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Oy 178 VGRGHGHTCSAVVKKGEYKGTVAVKTIKAKMTAISIEDVREVKILRALSGHNNLY 237
Db 162 VGRGHGHTCSALVKKGEYKGNAAVVKTIISKAKMTAISIEDVREVKILRALSGHNNLY 221
Oy 238 KRYDACCEGLNLYIYMECEGELLDRILARGRYTEEDAKAIYVQILSVAFCHLQGV 297
Db 222 KRYDACCEGLNLYIYMECEGELLDRILARGRYTEEDAKAIYVQILSVAFCHLQGV 281
Oy 298 HRDLKPENFLFTTRDENAPMKLIDGLSDPIRPERLNDIVGSAYVAPEVLHYSYMEA 357
Db 282 HRDLKPENFLFTTRDENAPMKLIDGLSDPIRPERLNDIVGSAYVAPEVLHYSYMEA 341
Oy 358 DIWSIGVITYILGSRPFWARTESGIFRSYLRADPNFDDSPWPSVSAEAKDFPKRLNK 417
Db 342 DIWSIGVITYILGSRPFWARTESGIFRSYLRADPNFDDSPWPSVSAEAKDFPKRLNK 401
Oy 418 DYRRMPTAVOALTHPMLRDEORQIPDLILFRILKQYLRAATPLKRLKALSKALREDEL 477
Db 402 DYRRMPTAVOALTHPMLRDEORQIPDLILFRILKQYLRAATPLKRLKALSKALREDEL 461
Oy 478 LYLKQFLKLEPRROGFSVLDNFRALTTRYLDAMKESVLEFLHALPEPLAVRRMDEEFC 537
Db 462 LYLKQFLKLEPRROGFSVLDNFRALTTRYLDAMKESVLEFLHALPEPLAVRRMDEEFC 521
Oy 538 AAASIPYOLEALEREWEIAGTAFQOEEOGNRVISVEELAOELNLAPTHYSIVQDMIRKS 597
Db 522 AAASIPYOLEALEREWEIAGTAFQOEEOGNRVISVEELAOELNLAPTHYSIVQDMIRKS 581
Oy 598 DGKLNFLGFTKFLHGVTIRGSNTRRH 623
Db 582 DGKLNFLGFTKFLHGVTIRGSNTRRH 607

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RESULT 3
B84906
probable calcium-dependent protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: B84906
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
J.; Guss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: B84906
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-595 <STO>
A:Cross-references: GB:AE002093; NID:g3831444; PIDN:ACG69927.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g46700
A:Map position: 2

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Query Match 66.8%; Score 2179; DB 2; Length 595;
Best Local Similarity 68.3%; Pred. No. 4.8e-76;
Matches 426; Conservative 71; Mismatches 93; Indels 34; Gaps 7;
Oy 1 MGOCYGRK-GASGRADDEGGVTEHQSPPPANGLPSTPRQQAQAQAQVGTPRRRGSKS 59
Db 1 MGOCYGRKVNQSKONGEENATTTYYVSGDNGIQPLT-----VNGRAKKNTPA 49
Oy 60 GSTPFGHQTGVAMPSPYPSGASPLPAGVSPSPAR-STPRFRFRPPPPPAKHAKAT 118
Db 50 RSSNPS-----PWSPPPHGASPLPAGVSPSPARSTPRFRFRPPPPPAKHAKA 103
Oy 119 LAKRLGGCKREKGTIPBEGGACAGAGGAGGAGADGAETPRDLKTTGFSKNGAKYELGKEV 178
Db 104 LAKRL-GVAKPRGRIPEE-----KGTPEOSLKSFGYGNFGAKYELGKEV 149
Oy 179 GRGHGHTCSAVVKKGEYKGTVAVKTIKAKMTAISIEDVREVKILRALSGHNNLYK 238
Db 179 GRGHGHTCSAVVKKGEYKGTVAVKTIKAKMTAISIEDVREVKILRALSGHNNLYK 238

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Db	150	GRGHEGHCSCGRGKGDIKDHPAVKIIISAKMPTAIEDVREXYLLKSJGHKYLK	209
Qy	239	FYDACEBGLNANYIWEIJCESGELLDRLLARGRYTEEDAKAIYQIILSYAFCHLOGVH	298
Db	210	YTDACEEDANNYYIWEIJCEDGELDRILLARGKYPEDDAKAIYQIILTVYFCHLOGVH	269
Qy	299	RDLPENPLFTTRDBNAPMKLIDFGLSDFIKPPDERLNDIVGSAIYYAPEVLHNSYMEAD	358
Db	270	RDLPENFLFTSSRSDSLKIDGLSDFIKPPDERLNDIVGSAIYYAPEVLHNSYLEAD	329
Qy	359	IMSIGVITYIILCCSRPMATTEGITSRSVLADPNFDDSPWIVSAEADPVKRFPLNKD	418
Db	330	IMSIGVIYYIILCCSRPFMATTEGIFRTVLTPEPNYDDVPWPSCESEGKDFVKRLNKD	389
Qy	419	YRKRTATVQALTHWLRDEQOIFLDLILFRLIKYQIRATPPLKRLAKLSKALREDELL	478
Db	390	YRKRSAAVQALTHWLRDSDSVIFLDLILIKYKAYLHAAPPLKRLAKLSKALKTENEIV	449
Qy	479	YLKIQFKLLER-RGCFVSLDNFRALTRYLTDAMKESRVEFLHALEPLAYRRMDPEFC	537
Db	450	YLRAQFMILGNKGSVLSLENFKALQMNATDAMRESRVEPLHTMESLAYRRMYPEFC	509
Qy	538	AAATSPVOLALEMEELAGTAFQFQFQEGNRVYSVELEAOELNATHTSIVODWTRKS	597
Db	510	AAATISHOLEAVNDAMEELATAGFHFETEGNRVITIEELARELVNGASAYGLRDWYRSS	569
Qy	598	DGKLNFLGFTKFLHGVITIRGSR 621	
Db	570	DGKLSYLGFTKFLHGVITIRAAHAR 593	

RESULT 4

T45842

calcium dependent protein kinase-like - Arabidopsis thaliana

N:Alternate names: protein F2K15.230

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 04-Feb-2000 #text_change 04-Mar-2000

C:Accession: T45842

R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000

A:Reference number: Z23015

A:Accession: T45842

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-594 <RIE>

A:Cross-references: EMBL:AL132956

A:Experimental source: cultivar Columbia; BAC clone F2K15

C:Genetics:

A:Map position: 3

A:Introns: 180/3; 224/2; 238/2; 274/3; 301/1; 400/1; 436/3; 471/3; 492/3; 548/3

A:Notes: F2K15.730

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match	60.4%	Score	1970	DB	2	Length	594
Best Local Similarity	62.8%	Pred.	No. 3,86	DB	2		
Matches	391	Conservative	81	Mismatches	117	Indels	34
				Gaps			8

QY	1	MGQCYGKGSAGTADDEGGVTEHOSPPRANGLPSTPRQQAQAQOQVTPRRRSGSG	60
		: : :	
Db	1	MCHCYSRNIPTVDDE-----IPs-----ATAADLPHRSHNNHQTSSS	39
QY	61	STTPHQRPGVAMPSPYP-SGGASPLPAGVSPSPASRTPRRFKRPSPRSAPKIKATL	119
		: : : : : : : : : : :	
Db	40	SSIP--QSASVEVNPYNISPPQSLPAGVAPSPAR-TPGRKFEMKPPSPSPAKPIAAL	96
QY	120	AKRLG-GGKPEKGTIPPEEGVAGVGGGGGADGAETERPDLKTFEFSKNFGAKYELGKEV	178
		: : : : : : : : : : :	
Db	97	RRRRGTAPRRPGRLPEDESEAGSGGGIG-----ER-LDKNFCPAKNEBEKYEELGREV	148
QY	179	GGHGHTCSAVYKKGEGYGVAVYKIIAKAKMTALISTEDYRREVKILRALSGHNNLYK	238
		: : : : : : : : : : :	
Db	149	GGHGHTCMAWAKGKGIKGQTVAVKIIISKSMTALSIEDVRREVKILKALSGSHMYK	208

QY	239	FYDCECDLANYIYMEICEGELLDRILARGRYTEDAKAIYVOILSYVAFCHJGCVH	298
Db	209	FYDVEEDSNVYVYMELCEGSELLDSTILARGRIPEAEAKRIYQIILSATAFHLJGCVH	268
QY	299	RDLPAPENFLFTTRDENAPMKLIDFGLSDFIRPDERLNDIVGSAYVAEYVLHRSYMEAD	358
Db	269	RDLRPENFLFTSKNEDAVALKYIDFGLSDYAFRDQLNDVYGSAYYVAEYVLHRSYSTHAD	328
QY	359	IMSIGVITYIILCCSRPMATBESGITSRSYVLRADPNFDDSSWPIVSAEADPFYKRLFNKD	418
Db	329	IMSIGVITYIILCCSRPPTGYTEBAIFRCYVLRAPNFDDELPPWPSIPSIADPFYKRLFNKD	388
QY	419	YRKRRATAVQALTHMLREDCQOIFLIDILIFRLIKQYRAPRLKATKALSKALREDELL	478
Db	389	HKRRATAQALAHMLRDNENGLLDDSTYKLVASYSIRASFPFRAALAKLSKALPEEELY	448
QY	479	YLKLOFKLLEBRDGFVSLDNFRITALTRYLDAMKESRYLEFLHALLEIDLAYRMDPEEFCA	538
Db	449	FLKQFMLEBREDGGHLHNHTTALTRATDAMIESTRLPDILNMQGLAKKIDLEEFCA	508
QY	539	VAISPYQLEALERMEDEIAGTAFQOPEOBGNRVISVEELAOELINAPHYISIVODMIRKSD	598
Db	509	ASVSYYQLEALEEMWEOIATVAFEFHFESEGSRAISVOELAEEMSGVAPNAYPLDKMIRSLD	568
QY	599	GLNLFGFTKFLHGVITNGSNTR	621
Db	569	GLNLFGLTAKFLHGVITNASSSR	591

RESULT 5

T46084

CDPK-related protein kinase - Arabidopsis thaliana

N:Alternate names: protein_T20E23.130

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Mar-2000

C:Accession: T46084

R:Barquès, M.; Perez-Perez, A.; Terol, J.; Torres, A.; Perez-Alonso, M.; Mewes, H.W.; Submitted to the Protein Sequence Database, December 1999

A:Reference number: 223020

A:Accession: T46084

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-601 <BAR>

A:Cross-references: EMBL:AL133363

A:Experimental source: cultivar Columbia; BAC clone T20E23

C:Genetics:

A:Map position: 3

A:Introns: 186/3; 230/2; 244/2; 280/3; 307/1; 406/1; 443/3; 479/3; 500/3; 556/3

A:Note: T20E23.130

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

	Query Match	Score	DB 2	Length	601
	Best Local Similarity	60.48	Pred. No.	3.8e-66	
	Matches	380	Conservative	87	Mismatches 116; Indels 46; Gaps
QY	1	MGQCYGKAGSGATDDEGGVYTEHOSPPANGLPST---	PPROAOAOAOQVCTPRRG	56	
	1	1	1	1	1
Db	1	MGICTSKENSSNS-----DOTPARANPLPASESVKSSSVNGEDDCCVYTTNNEG	50		
QY	57	SKSG-----STTPGHQTPGVAMPSPSYPGGASPLACVSPSPARSTRPRFRKRPFPSP	111		
	57	1	1	1	1
Db	51	KKSPFPPTSPSPAHYFFSKTKTPASPTFNST-----NSTKRRFFKRPFPSP	99		
QY	112	AKHIKATLAKRLGGCKPKPEGTIPBEGGVGAGGGGGAADGAETERPLDKTTFEFSKNGAK	171		
	112	1	1	1	1
Db	100	AKHIAVLAIRRHGSAVKPNSSAIPK-----GSEADGGGVG-----LDKSPGFSKSPASK	147		
QY	172	YELGKEVGRGHFGHTCSAVVKKGEKQOTYAVKIIAKAKMTAISIDVYREVYILAL	233		
	172	1	1	1	1
Db	148	YELGDEVGRGHFGYCAKPKKGDKKGOVAVKIIPAKMTTALAIDEVREYVILAL	207		

Qy	232	GHNNUYKRYDACEGOLNAYIMELCEBGEGLLDRLIARGRYTEEDAAIYVOLLSVAF	231
Db	208	GHNNUYKRYDACEGOLNAYIMELCEBGEGLLDRLIARGRYTEEDAAIYVOLLSVAF	267
Qy	292	HLGGVYHRRDLKPENFLFTTRBENAPMKLIDFGSDLFRPBERLNDIYGASVYAAPEVLR	351
Db	268	HLGGVYHRRDLKPENFLFTTRBENAPMKLIDFGSDLFRPBERLNDIYGASVYAAPEVLR	327
Qy	352	SYSMEDADWSIGVYTYILLGSGRPFARTEBSGIFRSVLADPNFEDSPWPTVSAEAKDFV	411
Db	328	SYSTEADWISGVYTYILLGSGRPFARTEBSGIFRAVLAKDPFDDPMPFLTSSERDFV	387
Qy	412	KRLPNKDYRKRYTAAVOALTHPHWMLD-BQORIPDILFEFLIKOYLATPFLKRLALAKLSK	470
Db	388	KRLPNKDYRKRYTAAVOALTHPHWMLD-BQORIPDILFEFLIKOYLATPFLKRLALAKLSK	447
Qy	471	ALRDELLYTLKLOEKLDEP-RDGFVSLDNERTALTRYLDAMKESRYLEFLHALEPLAYR	529
Db	448	TLTVDELFYLRGEGVALLPEPSKNGTISLENTKSKALMKKATDAMKDSRIPETLGLSALOIR	507
Qy	530	RMDEEFCFAAISFYQLEALERWEELIGTAPFOOPEQGNRVISVEELIAOELNLAFT--HY	587
Db	508	RMDEEFCFAAISFYQLEALERWEELIGTAPFOOPEQGNRVISVEELIAOELNLAFT--HY	567
Qy	588	SIYODWIRKSPDKNLNFGPFLKHLGVYIR	616
Db	568	AVLWMDLRRHDDGKLSLGEFVKYKLLHGVSSR	596

RESULT 6
S60052
calcium-dependent protein kinase homolog - carrot
C:Species: *Daucus carota* (carrot)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999
C:Accession: S60052
R:Lindzen, E.; Choi, J.H.
Plant MOL. Biol. 28, 785-797, 1995
A:Title: A carrot cDNA encoding an atypical protein kinase homologous to plant calcium-c
A:Reference number: S60052; MUID:95367641
A:Accession: S60052
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-602 <LIN>
A:Cross-references: EMBL:X83869; NID:g1103385; PIDD:CAA58750.1; PID:e135087; PID:g110338
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold
C:Keywords: ATP
F:146-410/Domain: protein kinase homology <KIN>
F:154-162/Region: protein kinase ATP-binding motif

[illegible]

Qy	297	VHRDLKPEHEFTTRDENA	PKMLIDFGSLDPIRDER	NDLVGSANYA	VPVLRHRS	5ME	356
Db	273	VHRDLKPEHEFTKSDDESO	SLKLDIDFGSDYVKKPER	INDLVGSAYVA	VPVLRHRS	5TE	333
Qy	357	ADIMSIGVTVYLLCGSR	PPMARTESGJFRSVLR	ADPFFDOSPMPYSAE	KDDVKKF	FLN	416
Db	333	ADVMISIGVSYLLCGSR	PPMARTESGJFRVAVL	KANLSFDEPPMPSVSE	KDDVKKFLN		392
Qy	417	KDYRRMTAVOALTRPML	RDEOR-QIPDLILFRLI	KOYLTRATPLKAL	KALSKALRED		475
Db	393	KDPRKRMATAQAOLCH	SWIKNSNDIKFRLDIL	VFKLMKYMSSPLR	KALRALSKTLTYD		455
Qy	476	ELLYLKLOFKLLER-RO	GFVSLDNRFLATLYT	LTDAMKESVYLEFL	HALERLAVRRMDFE		534
Db	453	ELFYKEGFVLLERPKNT	ISLENTKQALMRNSYD	AKDSVSRDLDLVS	LALQRRMDFE		512
Qy	535	EECAALIPYOLEALER	BEELAGTAFOOFBOE	BGRNVSVEELAQEL	MARP--HYSTYOD		592
Db	513	EECAALISVHOEALDR	MEQARCAVYDFEEDK	GNRAIMIEELASL	ELGSPVNAVLHD		572
Qy	593	WIRKSDGRLNFAGTK	FFLHGVYIR	616			
Db	573	WIRHTDKLSFLGYK	LLHGVSTR	596			

RESULT 7
T51264
calcium-dependent protein kinase-like - Arabidopsis thaliana
N:Alternate names: protein T8M16_90
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
C:Accession: T51264
R:Benes, V.; Wurmach, E.; Drzonek, R.; Ansoerge, W.; Mewes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, August 2000
A:Accession: T51264
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-577 <BEN>
A:Cross-references: EMBL:AL390921
A:Experimental source: cultivar Columbia; BAC clone T8M16
C:Genetics:
A:Map position: 3
A:Initrions: 162/3; 206/2; 220/2; 256/3; 283/1; 382/1; 419/3; 455/3; 476/3; 532/3
A:Note: T8M16_90
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

Query Match	56.1%;	Score 1829;	DB 2;	Length 577;
Best Local Similarity	56.7%;	Pred. No. 7.8e-63;		
Matches 355;	Conservative 100;	Mismatches 107;	Indels 64;	Gaps 7.
QY	1	MGCGKAGKASGR	TADDEGGVTEH	OSPSPANLSTPT
Db	1	MGCLCHK	-----PIEQSNLPI	SNIEETPKNNSSOKANS-----35
QY	61	STTPGHQTPGVAMP	SPYPSGASPLPA	-----GVSPPASPTPRFRFP
Db	36	-----	SGPFYSPSPPLSLFK	SPASVSSSVSTPLRIKRRPPSPAKH81
QY	115	IKATLAKRLGGGK	REKEGIIPEBGGV	GAGGGGGAADGAE
Db	82	IRALLARHGGVSK	MEASISPE-----	GSECEVGLDKKGFSGKOFASHYE126
QY	175	GKEVGRGHFGHTC	SAVYAKKGEYKGT	QAVAKIIAKAKMTTALSIE
Db	127	DGEVGRGHFGYTC	SAKKGSLKGDVAV	KVYIPKSKMTTALAI
QY	235	NLVEFYACCEGLN	WYIIMELCEGGEL	DLRLANGRTTEDAKAI
Db	187	NLVPFTADFEDE	NVYIIMELCGGEL	DLRLANGRTTEDAKAI

Query Match	35.4%;	Score 1153.5;	DB 2;	Length 571;
Best Local Similarity	40.8%;	Pred. No. 2.6e-37;		
Matches 257;	Conservative 103;	Mismatches 191;	Indels 79;	Gaps 11

Db 531 EADIDNDGKISLQEFFRRLRLTASIKSRNVR 560

Db 531 EADIDNDGKISLQEFFRRLRLTASIKSRNVR 560

Query Match 33.1%; Score 1080; DB 2; Length 536

QY 110 SPARKHAKTLAKRLGGKPKKEGTIPREGGVAGGGGGAADGATERPLDKTFTGSKNFG 169
 Db 62 VVAP-----PKPTPTD-----GKLT---DVR 82
 QY 170 AKELGKEVGRGHNT--CSAVVKKGEYKQGVAVAKIATAKMTAISIENVREKTL 227
 Db 83 SVSLKEKEKRGQGVYLTCTEIA-----SGKQACKSKSKRLVSKAKEDIRREIQIM 137
 QY 228 RALSGNNLVKVEDACEDGLNIVYIWELECGELDRILARCGRTEDAKAIIVOILSV 287
 Db 138 QHLSGQONIVFRGATEDNSNVHVMELCAGELFDRITAK--GHYSERAAATICRAVNV 196
 QY 288 VAECHLQGVVHRDLKPENEFTTRDENAPMKLIDFGLSFIPDELDNIVGSAVYVPE 347
 Db 197 VNICHFMGVVHRDLKPENEFTTRDENAPMKLIDFGLSFIPDELDNIVGSAVYVPE 256
 QY 348 VLRHSYSMADWISGVITYIILCSRPFWARTESGIFRSVLRADPNFDSFPTVSAEA 407
 Db 257 VLARNYKGEIDVWSAGVILYILSGVPFWAETEGKIFDALOGELDESPQWPSISSA 316
 QY 408 KDFVRFLLKDYRKRTAVQALTHPLRD--EQROIPLDILFRLLKQYLKATPLKRLAK 466
 Db 317 KDLVRKMLDQPKRTTSQVLOHPLNDGEASDKPIDSAVLSRKQFRANMKLKAKLK 376
 QY 467 ALSKALREBELLYLKQFKLE--PRDGFVSLDNFTALTRYLTDAKESRYLEFLHALEP 525
 Db 377 VLASNLNEEIKGLQKMFNDMTDNGSTIYEELKAGLAK--LGSRLSAEYKQLEMAVY 435
 QY 526 LAYRRMDFEEFCAAAIISPOLALERMELIAGTAQOFEQGNRVISVEL-----AOEL 580
 Db 436 DENGSDIVYEFTTATMHRKLER---DEHLKAFQYFDKDNSTGTRDELSALIEHEM 491
 QY 581 NLAPHYSIVODWIRKSDGKLNFLGFTKPLNG 612
 Db 492 GDTSTIKDIISEVDTDNDGRINYEFCAMRG 523

RESULT 14

S71774

calcium-dependent protein kinase (EC 2.7.1.-) 6 - Arabidopsis thaliana
 N:Alternate names: protein F9D16.120
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 14-May-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999

C:Accession: T05597; S71774; S71901; S71197
 R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Chua, N.H.
 submitted to the Protein Sequence Database, February 1999

A:Reference number: Z15419
 A:Accession: T05597

A:Molecule type: DNA

A:Residues: 1-529 <BEV>

A:Cross-references: EMBL:AL05394

A:Experimental source: Cultivar Columbia; BAC clone F9D16

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Chua, N.H.
 Plant Mol. Biol. 30, 1259-1275, 1996

A:Title: Expression of three members of the calcium-dependent protein kinase gene family

A:Reference number: S71774; MUID:96311013

A:Accession: S71774

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1448, 'K', 450-529 <HON>

A:Cross-references: EMBL:U20625

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N.
 submitted to the EMBL Data Library, February 1995

A:Description: Expression of the calcium-dependent protein kinase gene family in Arabid

A:Reference number: S71197

A:Accession: S71901

A:Molecule type: DNA

A:Residues: 1-529 <HOA>

A:Cross-references: EMBL:U20625; NID:9836943; PIDN:AAA67656.1; PID:9836944

A:Accession: S71197

A:Molecule type: mRNA

A:Residues: 1-529 <HOW>

A:Cross-references: EMBL:U20623; NID:9836939; PIDN:AAA67654.1; PID:9836940
 C:Genetics:
 A:Gene: CDPK6
 A:Map position: 4
 A:Note: 137/2; 233/1; 281/1; 332/1; 370/3; 426/3; 469/2; 502/3
 C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein
 F:76-336/Domain: protein kinase homology <KIN>
 F:84-92/Region: protein kinase ATP-binding motif
 F:379-411/Domain: calmodulin repeat homology <EF1>
 F:451-483/Domain: calmodulin repeat homology <EF2>
 F:483-518/Domain: calmodulin repeat homology <EF3>
 F:107/Active site: lys #status predicted

Query Match 27.7%; Score 903.5; DB 1; Length 529;
 Best Local Similarity 39.5%; Pred. No. 6, 9e-28;
 Matches 209; Conservative 91; Mismatches 178; Indels 51; Gaps 14;

QY 107 PPSPAR-----HIKATLAKRLGGKPKKEGTIPREGGVAGGGGGA-----DGAE 153
 Db 13 PPSSSSSSGNVVNHVKKRAGER--GSSGSGT---GSSGSGTGSNSTSTQONGRI 66
 QY 154 TERPLDTFGSKNFGEKYLGEVGRGHGHTCSAVVKKGEYKQGVAVAKIATAKMTT 213
 Db 67 LGRMEEV-----RRTYFEGRELGGQGVYLVYTHKETK---QGVACKSIPTRLV 116
 QY 214 AISTEDYRREKTLRALSGNNLVKFPYDCEDELNIVYIWELECGELDRILARCGRT 273
 Db 117 KDIEDYRREVOIMHLSGHRNTVDLKGAYEDNSVNLWELECGELDRITLTK--GLYS 175
 QY 274 EDAKAIIVOILSVAFCHLQGVVHRDLKPENEFTTRDENAPMKLIDFGLSDFTRPDER 333
 Db 176 ERAAADLCROMVNVVHSCSMGVHRDLKPENEFTLSDKNSPLKTDGSLVFEPKPGK 235
 QY 334 LNDIVGSAVYVAREVLRHSYSMADWISGVITYIILCSRPFWARTESGIFRSVLRADP 393
 Db 236 FKLVSATYVAREVLRKNTGPRADWSAGVILYILSGVPFWAETEGKIFDALOGEL 295
 QY 394 NFDSDFWPTVSABAKDFVRFNKDYRKRYTAVQALTHPLMD--EQROIPLDILFRLL 451
 Db 296 DFGADWPALSDQAKDLVRKMLKYDPKRLTAENVLHNPWEDEASDKPLDNVLSRM 355
 QY 452 KQYLRTPYKRLAKRLSKALREDELLYKLOFKLE--PRDGFVSLDNFTALTRYLTDA 510
 Db 356 KQFRANMKLKAKLVIAENLSEEBITGLKEFKSLTDNNIGVTLLELRITGLPK--LGSK 414
 QY 511 MKESRYLEFLHALEPLAYRRMDFEEFCAAAIISPOLALERMELIAGTAQOFEQGNRV 570
 Db 415 ISEAEIRQLEMAADNDGOSIDYLEFISNTM---HNNTER-EDLYLAFTAFDNDNSGY 470
 QY 571 ISVEELAGLNLAPHYSIVODWIRKS-----DGKLNFLGFTKPL 610
 Db 471 TWE-----ELFLAMKRYNWDGDKSIKEITAEVDTDRDKINYEFEVAM 515

RESULT 15

T09940

calcium-dependent protein kinase (EC 2.7.1.-) CDPK - pumpkin

N:Alternate names: calcium-dependent calmodulin-independent protein kinase CDPK

C:Species: Cucurbita pepo (pumpkin)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T09940

R:Ellard-Ivey, M.; Hopkins, R.B.; White, T.J.; Lomax, T.L.
 Plant Mol. Biol. 39, 199-208, 1999

A:Title: Cloning, expression and N-terminal myristoylation of CDPK1, a calcium-depen

A:Reference number: Z16998; MUID:9918773

A:Accession: T09940

A>Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-573 <ELL>

A:Cross-references: EMBL:U90262; NID:g1899174; PIDN:AAB49984.1; PID:g1899175

A:Experimental source: etiolated hypocotyls

C:Genetics:

A:Gene: CPK1

C:Function:

A:Description: serine/threonine-specific protein kinase activated by direct binding of C:
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C:Keywords: ATP; calcium binding; EF hand; membrane protein; myristylation; phosphotrans
F:108-368/Domain: protein kinase homology <KIN>
F:447-479/Domain: calmodulin repeat homology <EFH>

```

Query Match          27.5%; Score 895.5; DB 2; Length 573;
Best Local Similarity 36.6%; Pred. No. 1.5e-27;
Matches 207; Conservative 98; Mismatches 205; Indels 55; Gaps 13;

QY 57 SKSGSTTPGHTPGVAMPSPYPPGASPLPACVSPSPARSTPRFRFRPPPPAKHK 116
   11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 26 SKTPENSVSHTNGENREYVASEPSPLPVQNP-PEKVTMPESVAKPPPEPKYR-- 82
   26 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 117 ATLAKRLGGCKPKRGTPREBGGVAGGGGGAADGAEETERPLDKTFGFSKNFGAKYELGK 176
   83 -----PVAKRVSAGLRGGSVLTQKT-----GNFKETYSLGK 114
   83 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 177 EVGRGHGHTCSAVKKGEYKQTVAVKIIAKAKMTAISIEDVRRREVKILRALSGHNL 236
   115 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 115 KLAGOGFGTTYMCVEKA---TGKEYACKSIARKRLVNEDVEDVREIQIMHLSGHPNV 171
   115 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 237 VKFYDACCEDLNYIYVIELDEGGELDRILARGRYTEEDAKAVQILSVAFCHLGQV 296
   172 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 172 ISTKGAEEDVAOVVVELCAGGELFDRIQR-GHYTERKAELTRTVGVLEACHALGV 230
   172 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 297 VHRDLKRENFLFTTRDENAMPKLIDFGLSDFIRPDERLNDIVGSAYVAPVLRHSYSME 356
   231 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 231 MHRDLKRENFLFSKEESLTKTIDFGLSMFKRGEKFNQVGSPPYVAREVLKRGPE 290
   231 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 357 ADIWSIGVTIYILLCGRPFRTWARTESGIFRSVLRADPNFDDSPWPTVSADAKDFVKRFLN 416
   291 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 291 ADVWSAGVIYIILSGVPPWASEEGIFEEVYLGDLDFSSDPWPSISDSKDLVRRMLV 350
   291 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 417 KDYRKRTAVOALTHPWLRLDE--QRQIPLDILIPRLIKOYLRAATPLKRLALKALSKALRE 474
   351 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 351 RDRPKRLTAEVLCHPWVQVADGVAADPKLDLSAVLTRLKQFSAMNKLKKMAIKVIAESLSE 410
   351 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 475 DELLYLKIQFKLLE-PRDGEVSLDNFRTALTRYLTDMAKESRVLEFLALEPLAYRRMDP 533
   411 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 411 EETAGLKEMFKMIDTDSGQITFEELKAGLKKFGAN-LKSEIYDLMOAADIDNNGTIDY 469
   411 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 534 EEFCAAAISPYOLEALERWEEIAGTAFQPEQEGNRIYSVEELAQELNLAPTHYST---- 589
   470 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 470 GEFYAATL--HINKIEKEHLL-AAFSYFDKDSGFTIHDELQ---ACKKEGIEDLQ 521
   470 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 590 VQDMIRK----SDGKLNFLGFTKFL 610
   522 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 522 MEEMREVDQNDGSDIDYNEFVAMM 546
   522 : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: May 2, 2002, 08:37:27
Job time: 7931 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2002, 08:40:21 ; Search time 71.84 Seconds
(without alignments)
317.959 Million cell updates/sec

Title: US-09-854-731-4

Perfect score: 3260

Sequence: 1 MGCCYGCAGSRTADDEGV.....LGFTKFLHGVIRGSTRRH 623

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1894	58.1	602	1 CRK_DAUCA	P53661 daucus caro
2	904.5	27.7	533	1 CDP2_ORYSA	P53663 oryza sativ
3	877	26.9	610	1 CDP1_ARATH	Q06850 arabidopsis
4	865	26.5	513	1 CDP2_MAIZE	P49101 zea mays (m
5	847.5	26.0	532	1 CDPK_DAUCA	P28582 daucus caro
6	817	25.1	508	1 CDPK_SORBN	P28583 glycine max
7	794	24.4	542	1 CDP3_ORISA	P53662 oryza sativ
8	747	22.9	534	1 CDP1_ORYSA	P53662 oryza sativ
9	505.5	15.5	370	1 KCC1_HUMAN	Q14012 homo sapien
10	505.5	15.4	374	1 KCC1_HUMAN	Q63450 rattus norv
11	501	15.5	469	1 KCC4_MOUSE	P08414 mus musculu
12	498	15.3	295	1 KMLC_DICDI	P25323 dictyostell
13	495	15.2	474	1 KCC4_RAT	P13234 rattus norv
14	493.5	15.1	446	1 KCC1_YEAST	P27466 saccharomyc
15	490	15.0	473	1 KCC4_HUMAN	Q16566 homo sapien
16	486	14.9	533	1 KCCD_RAT	P15751 rattus norv
17	484	14.8	499	1 KCCD_HUMAN	Q13557 homo sapien
18	470	14.4	1431	1 DAPK_HUMAN	P53355 homo sapien
19	467.5	14.3	478	1 KCCB_RAT	P11275 rattus norv
20	464.5	14.2	478	1 KCCA_MOUSE	P11798 mus musculu
21	463.5	14.2	512	1 KII1_ARATH	Q38997 arabidopsis
22	461	14.1	607	1 KMLC_RABIT	P07313 oryctolagus
23	461	14.1	740	1 DCK1_HUMAN	Q15075 homo sapien
24	460.5	14.1	414	1 KCC1_EMENT	P00071 emeticella
25	458	14.0	542	1 KCCB_MOUSE	P28652 mus musculu
26	455.5	14.0	609	1 KMLC_RAT	P20689 rattus norv
27	455	13.9	542	1 KCCB_RAT	P08413 rattus norv
28	454	13.9	447	1 KCC2_YEAST	P22517 saccharomyc
29	451.5	13.8	335	1 KCC1_SCHPO	Q9P712 schistosach
30	448	13.7	406	1 KPBH_HUMAN	P15735 homo sapien
31	448	13.7	433	1 DCK1_RAT	Q08875 rattus norv
32	447	13.7	664	1 KCCB_HUMAN	Q13554 homo sapien
33	444.5	13.6	386	1 KPBG_HUMAN	Q16816 homo sapien

34	443	13.6	382	1 KCC1_MEFAN	Q14408 metarhizium
35	440.5	13.5	406	1 KPBH_RAT	P31325 rattus norv
36	438.5	13.5	386	1 KPBG_RABIT	P00518 oryctolagus
37	438.5	13.5	397	1 S17A_RABIT	Q9gm70 oryctolagus
38	436.5	13.4	527	1 KCCG_RAT	P11730 rattus norv
39	434.5	13.3	387	1 KPBG_RAT	P13286 rattus norv
40	429	13.2	733	1 K6AA_XENLA	P10665 xenopus lae
41	429	13.2	1906	1 KMS_CHICK	P11799 gallus gall
42	427.5	13.1	415	1 KCCS_MALDO	Q07250 malus domes
43	427.5	13.1	1176	1 KMS_BOVIN	Q28824 bos taurus
44	424.5	13.0	387	1 KPBG_MOUSE	P07934 mus musculu
45	424.5	13.0	414	1 S17A_HUMAN	Q9uee5 homo sapien

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	602 AA.
CRK_DAUCA				
ID	CRK_DAUCA			
AC	P53661;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DE	CDPK-RELATED PROTEIN KINASE (EC 2.7.1.-) (PKA21).			
GN	CRK.			
OS	Daucus carota (Carrot).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Asteridae; euasterids II; Apiales; Apiaceae; Daucus.			
OX	NCBI_TaxID=4039;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. JUMAROT;			
RX	MEDLINE=95367641; PubMed=7640352;			
RA	Lindzen E., Choi J.H.;			
RT	"A carrot cDNA encoding an atypical protein kinase homologous to			
RT	plant calcium-dependent protein kinases."			
PL	Plant Mol. Biol. 28:785-797(1995).			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	CAMK SUBFAMILY.			
CC	-1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS. ALL SEEMS			
CC	NON FUNCTIONAL.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
CC	EMBL: X83869; CA56750.1; -			
DR	HSSP: Q63450; 1A06.			
DR	InterPro: IPR002048; EF-hand.			
DR	InterPro: IPR000719; Euk_pkinase.			
DR	InterPro: IPR002290; Ser_thr_kin_actsite.			
DR	Pfam: PR00069; pkinase.1.			
DR	SMART: SM00220; S_TKc.1.			
DR	PROSITE: PS00107; PROTEIN_KINASE_APP.1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_ST.1.			
DR	PROSITE: PSS0011; PROTEIN_KINASE_DOM.1.			
KW	Transferase; serine/threonine-protein kinase; ATP-binding;			
KW	Repeat.			
FT	DOMAIN	20	40	3 X 7 AA TANDEN REPEATS OF S-[LI]-P-X-X-
FT	REPEAT	20	26	D-X.
FT	REPEAT	27	33	1.
FT	REPEAT	34	40	3.
FT	DOMAIN	148	410	PROTEIN KINASE.
FT	NP_BIND	154	162	ATP (BY SIMILARITY).
FT	BINDING	180	180	ATP (BY SIMILARITY).
FT	ACT_SITE	276	276	BY SIMILARITY.

FT DOMAIN 465 476 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
 FT DOMAIN 502 513 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
 FT DOMAIN 542 553 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
 FT DOMAIN 574 585 ANCESTRAL CALCIUM SITE 4 (POTENTIAL).
 SO SEQUENCE 602 AA: 67184 MM: 1D10BF68B7BF447 CRC64;

Query Match 58.1%; Score 1894; DB 1; Length 602;
 Best Local Similarity 60.4%; Pred. No. 1.9e-92;
 Matches 377; Conservative 89; Mismatches 122; Indels 36; Gaps 10;

QY 1 MGICVSK-----PSPEDPLHMHHTSIPIYND--TSLRP-QDNISIPKDLAIADQDNK-- 49
 DB 1 MGICVSK-----PSPEDPLHMHHTSIPIYND--TSLRP-QDNISIPKDLAIADQDNK-- 49
 QY 61 STTPGHQGTGVAMPSPYPS-----GASPLPAGVSPSPASTRRFRFRFPSPAKHKK 116
 DB 50 --PPGKSKFPLPPYSPSPAHFLFESKSPVAGSPAGSSNSTKRLE--PEPPSPAKHKK 105
 QY 117 ATLAKLGGKREKTEPIPEGVGAGGGGAADGAETERPDKTFEFSKNGAKAYELGK 176
 DB 106 AAMARRHGVSKNEAIPAIPENNEDVGAG-----LDKSFSGSKNGKSFEEVGE 152
 QY 177 EYGRGHFGHTGSAVVKKGYKQYVAVKIAAKMTAISIEDVREVKILRALSGHNL 236
 DB 153 EYGRGHFGHTGSAVVKKGYKQYVAVKIAAKMTAISIEDVREVKILRALSGHNL 212
 QY 237 VKEFYDACEGLNVIYVMEICEGELDLRIILANGRYTEEDAKAIYVOLLNVAAPCHLOGV 296
 DB 213 VOFYDAFEDHTNVIYVMEICEGELDLRIILANGRYTEEDAKAIYVOLLNVAAPCHLOGV 272
 QY 297 VHRDLKPEFLEFTRDENAPMKLIDFGLSDFTRPDERLNDIVGSAVYVAPEVLRKSYME 356
 DB 273 VHRDLKPEFLEFTRDENAPMKLIDFGLSDFTRPDERLNDIVGSAVYVAPEVLRKSYME 332
 QY 357 ADINSIGVITTYLLCGSPBPFAARTEGSEFRVLRADPFDDSPMPTVSAEKDQVKKFLN 416
 DB 333 ADVMSIGVITTYLLCGSPBPFAARTEGSEFRVLRADPFDDSPMPTVSAEKDQVKKFLN 392
 QY 417 KDYRRMTAVOALTHPMLRDEOR-QIPDLILFRILKOYLATPLKRLATKALSKALRED 475
 DB 393 KDYRRMTAVOALTHPMLRDEOR-QIPDLILFRILKOYLATPLKRLATKALSKALRED 452
 QY 476 ELVYLKLOFKLLEP-ROSFVSLDNFRALTRYLTDANKESVLEFLHALLEPLAYRRMDFE 534
 DB 453 ELVYLKLOFKLLEP-ROSFVSLDNFRALTRYLTDANKESVLEFLHALLEPLAYRRMDFE 512
 QY 535 EFCAAAISPYOLEALERMEIAGTAFOQFQEGNRSVSEVLELAQELNLP--HYSIVOD 592
 DB 513 EFCAAAISPYOLEALERMEIAGTAFOQFQEGNRSVSEVLELAQELNLP--HYSIVOD 572
 QY 593 WIRSDCKLNLGFTKFLHGVYTR 616
 DB 573 WIRSDCKLNLGFTKFLHGVYTR 596

RESULT 2
 CDP2.ORYSA
 ID CDP2.ORYSA STANDARD; PRT: 533 AA.
 AC P53683;

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 2 (EC 2.7.1.-) (CDP2.2).
 GN CPK2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. ARBORIO; TISSUE=Coleoptile;

RX MEDLINE-95284352; PubMed-7766885;
 RA Breviario D., Morello L., Giant S.;
 RT "Molecular cloning of two novel rice cDNA sequences encoding putative
 RT calcium-dependent protein kinases."
 RL Plant Mol. Biol. 27:953-967(1995).
 CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
 CC INVOLVE CALCIUM AS A SECOND MESSENGER.
 CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
 CC -1- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAWK SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC EMBL; X81394; CAA57157.1; -
 CC HSSP; Q63450; 1A06.
 CC Interpro: IPR002048; EF-hand.
 CC Interpro: IPR000719; Euk_Pkinase.
 CC Interpro: IPR002290; Ser_thr_kin_actsite.
 CC Pfam: Pf00036; efhand; 4.
 CC Pfam: Pf00069; pkinase; 1.
 CC SMART; SM00054; EFR; 4.
 CC SMART; SM00220; S_TKc; 1.
 CC PROSITE: PS0018; EF_HAND; 4.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 CC Calcium-binding; Phosphorylation; Multisubstrate family.
 CC FT DOMAIN 85 343
 CC FT NP_BIND 91 99
 CC FT BINDING 114 114
 CC FT ACT_SITE 209 209
 CC FT CA_BIND 398 409
 CC FT CA_BIND 434 445
 CC FT CA_BIND 470 481
 CC FT CA_BIND 505 516
 CC SO SEQUENCE 533 AA: 59522 MM: D0BC570ABD285E28 CRC64;

Query Match 27.7%; Score 904.5; DB 1; Length 533;
 Best Local Similarity 36.7%; Pred. No. 1e-40;
 Matches 210; Conservative 91; Mismatches 194; Indels 77; Gaps 14;

QY 55 RGSKSG-----STTPGHQGTGVAMPSPYPSGASPLPAGVSPSPASTRRFRFRFPSPAKHKK 109
 DB 15 RGSKSG-----STTPGHQGTGVAMPSPYPSGASPLPAGVSPSPASTRRFRFRFPSPAKHKK 109
 QY 110 SPKHKIKATLAKRLGGKREKTEPIPEGVGAGGGGAADGAETERPDKTFEFSKNGK 169
 DB 62 VVAP-----PKRTPPTI-----LGKLY--DVR 82
 QY 170 AKYELGKREKREKTEPIPEGVGAGGGGAADGAETERPDKTFEFSKNGK 227
 DB 83 AKYELGKREKREKTEPIPEGVGAGGGGAADGAETERPDKTFEFSKNGK 227
 QY 228 RALSGHNNLVKRYDACEGLNVIYVMEICEGELDLRIILANGRYTEEDAKAIYVOLLNVA 287
 DB 138 RALSGHNNLVKRYDACEGLNVIYVMEICEGELDLRIILANGRYTEEDAKAIYVOLLNVA 287
 QY 288 VAECFLGVHRDLKPEFLEFTRDENAPMKLIDFGLSDFTRPDERLNDIVGSAVYVAPE 347
 DB 197 VAECFLGVHRDLKPEFLEFTRDENAPMKLIDFGLSDFTRPDERLNDIVGSAVYVAPE 347
 QY 348 VLHRSYMEADIVSGVITTYLLCGSPBPFAARTEGSEFRVLRADPFDDSPMPTVSAEA 407
 DB 197 VLHRSYMEADIVSGVITTYLLCGSPBPFAARTEGSEFRVLRADPFDDSPMPTVSAEA 407

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Db 257 VLNRNNGKEIDVMSAGVILYLLSGVPPPEWAEETKEGIFDAILLOGEIDFESQPMPSISESA 316
OY 408 KDEVKEPLNKDYKRMATAVOALFHPMLRD-EQROIPDLILFRLIKOYLATPLKRLAK 466
Db 317 KDEVRKMLTODPKRITTSQVLOHPMLRDSADKPLDSAVLSRMKOFKAMNKLKMAK 376
OY 467 ALSKALREDELTYLKLOFKLLE-PRDGFVSLDNFRALFRTYLDAMKESVLEFLHALP 525
Db 377 VLSNLSNEEIKGLKQMTFMDTDSNGTITYEELKAGLAK-LSKSLSEAVKQLEADY 435
OY 526 LAYRRMDFEEFCAAISPYOLEALERMEEIAGTAFOQFEGEGNRVISEEL-AAAAEL 580
Db 436 DNGSDIDYEFITATNHRHLER----DEHLFKAFOYFKDKNSGTFRDELSALIEHEM 491
OY 581 NLAPFHYSTVQDMIRKSDGKLNFLGFTKFLHG 612
Db 492 GDTSTIKDITISEVDNDGRINTEFCAMARG 523

RESULT 3
CDP2_LARATH STANDARD: PRT; 610 AA.
AC 006850;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALCIUM-DEPENDENT PROTEIN KINASE, ISOBFORM AK1 (EC 2.7.1.-) (CDPK).
GN AK1 OR AT5G04870 OR MUK11.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLOMBIA;
RC MEDLINE=93213795; PubMed=7916621;
RA Harper J.F., Binder B.M., Sussman M.R.;
RT "Calcium and lipid regulation of an Arabidopsis protein kinase
RT expressed in Escherichia coli."
RT Biochemistry 32:3282-3290(1993).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. COLOMBIA;
RX MEDLINE=98162728; PubMed=9501997;
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RT DNA Res. 4:401-414(1997).
RL
CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY
CC PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -1- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN MOUSE-EAR
CC CRESS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC
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CC or send an email to license@isb-sib.ch).
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DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PR00036; ehand; 4.
DR Pfam: PR00069; pkInase; 1.
DR SMART: SM00054; EFh; 4.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00018; EF_HAND; 4.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation; Multigene family.
FT DOMAIN 150 408 PROTEIN KINASE.
FT BINDING 156 164 ATP (BY SIMILARITY).
FT BINDING 179 179 ATP (BY SIMILARITY).
FT ACT_SITE 274 274 BY SIMILARITY.
FT CA_BIND 464 475 EF-HAND 1 (POTENTIAL).
FT CA_BIND 500 511 EF-HAND 2 (POTENTIAL).
FT CA_BIND 536 547 EF-HAND 3 (POTENTIAL).
FT CA_BIND 570 581 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 610 AA; 68253 MW; 41868DF12B0DF9FB CRC64;

Query Match 26.9%; Score 877; DB 1; Length 610;
Best local Similarity 37.5%; Pred. No. 3.2e-39;
Matches 196; Conservative 98; Mismatches 179; Indels 50; Gaps 12;

OY 104 RPPPP--PSPAKHIAKATLARRLGGKPKKESTIPBGGVGAGGGGGAADCAETERPDKT 161
Db 112 KPDPAPKPKPKHMKRY-----SSAGLRRESVQRK 142
OY 162 FGFSKNGCAVEYLGCKEGRGHFGHTCSAVYKKGQVAVKIAAKMTAISIDVR 221
Db 143 ---TENKFEYSIGRKLGQGFITPLCEVET---TKERACKSIARKLITDVEDVR 196
OY 222 REVKILRALSGHNNLVKFYACEDGLNVYIVMELCEGELDLRLIARGRYTEDAKAY 281
Db 197 REIDIMHNLGHPVIVISIKGAEVDYAVHLVMECCAGELFDRIQR-GHYTEKKAELT 255
OY 282 VQILSVAFCHLQGVVRDLKPKENFLFTTRDENAPMKLIDFGLSDFTRPDERLNDIYGA 341
Db 256 RTIVGVVEACHSLGVMRDLPENFLFVSKHEDSLTITDFGLSMFPKPDVDFDVVGGSP 315
OY 342 YVVAPEVLHYSMEADLWSIGVTYILLGSRPFMAKRTSGIRSVLRADPNFDSPPM 401
Db 316 YVVAPEVLKRYKGPEDAVMSAGVIVYLLSGVPPPEWAEETEGIEQVLRHGLDSSDPMP 375
OY 402 TVSAEAKDFVKRFLNKDYKRMATAVOALFHPMLRDE--QROIPDLILFRLIKOYLRA 459
Db 376 SISESADIVRKMLVRDPKRLTAHQVLCHEWVQDVAPDKPLDSAVLSRMKOFKAMN 435
OY 460 LKRLALALSALREDELTYLKLOFKLLE-PRDGFVSLDNFRALFRTYLDAMKESVLE 518
Db 436 FKKAALRVIAESLEBEIAGIKEMFNMDADKSOITFEELKALKRGAAL-LKESEL 494
OY 519 FLHALPELAYRRMDFEEFCAAISPYOLEALERMEEIAGTAFOQFEGEGNRVISEELAQ 578
Db 495 LMQAADVNSGTIDYKEFIATL---HLNKIER-EDHLFAAFYFDKDGSGYITPDELQ 550
OY 579 ---ELNLAPFHY-SIVQDMIRKSDGKLNFLGFTKFLHGVTIRG 617
Db 551 ACEFGEVDVIEELMRVDQDNDGRIDYNEFVAMQSGSITG 593

RESULT 4
CDP2_MAIZE STANDARD: PRT; 513 AA.
AC P49101;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALCIUM-DEPENDENT PROTEIN KINASE 2 (EC 2.7.1.-) (CDPK 2).
```

GN CDPK2.
OS Zea mays (Maize).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
OC Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae: PACC clade;
OC Panicoideae: Andropogoneae: Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MERRIT. TISSUE=Root tip;
RX MEDLINE=95281563; PubMed=7761420;
RA Patis S., Takeawa D., Pooviah B.W.;
RT "Chimeric plant calcium/calmodulin-dependent protein kinase gene with
RL a neutral vishin-like calcium-binding domain."
Proc. Natl. Acad. Sci. U.S.A. 92:4897-4901(1995).
CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC AUTOPHOSPHORYLATION MAY PLAY AN IMPORTANT ROLE IN THE REGULATION
CC OF THE KINASE ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC -----
DR EMBL: U28376; AAA69507.1; -
DR HSSP: Q63450; 1A06.
DR MaizeDB: 56895; -
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk.pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00036; ehand; 4.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00054; EFh; 4.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00018; EF_HAND; 4.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation.
FT DOMAIN 65 323
FT NP_BIND 71 79
FT BINDING 94 94
FT ACT_SITE 189 189
FT CA_BIND 379 390
FT CA_BIND 415 426
FT CA_BIND 451 462
FT CA_BIND 486 497
SQ SEQUENCE 513 AA; 58081 MW; 235A61630CAC36 CRC64;

Query Match 26.5%; Score 865; DB 1; Length 513;
Best Local Similarity 37.0%; Pred. No. 1, le-38;
Matches 194; Conservative 92; Mismatches 198; Indels 40; Gaps 10;

DB 11 RRKRLRYNPPQAAEVRTPSATNSAVPVAVPP-----PTADTLL 54
QY 99 RREFKRPFPSPAKHKLAKRLGGKPKKEGTPEEGVGAGGGGAGDAAEFERPL 158
DB 11 RRKRLRYNPPQAAEVRTPSATNSAVPVAVPP-----PTADTLL 54
QY 159 DKRGESKNGANYELGKGVGHFGHT--CSAVVKKGEKQGVAVKTIKAKKTTAIS 216
DB 55 GKQY---EDVRSYYSFGKELRGQFGVTVLCTEIA-----SGQVYCKSKSRKLVSKAD 106
QY 217 IEDVREVKIPLALSGHNNLVKRYDCCEGLNVIYMELCGEGELLDRILARGRATVED 276
DB 107 REDIRREIOMHLSQPINVEFRGAYEDKSNVHVMELCAGGELFDRIIAK-GHYTERA 165

QY 277 AKAIWOLISVAFCHLOGVVRHDLKPNPFLTTREDNAPKLLIDFGLSDFIRDERLND 336
DB 166 AATIGRAVYNNVYNICHGVMWRDLKPNPFLATTEENAMKADFGLSVEITECKMYRD 225
QY 337 IVGSAVYVAPEVLYRSYSMEADIVSIGVITYILLGCSPPFMAETESGFJRVLRADPNF 396
DB 226 IVGSAVYVAPEVLYRSYSMEADIVSIGVITYILLGCSPPFMAETESGFJRVLRADPNF 285
QY 397 DSPMFTVAEAKEDPYKRLNMDYKRMATVAVALLHPWLRD--EDROIPDLTIFRLIKQY 454
DB 266 SOPWFSISESKADLVKRLTDPKRLTSAGVLOHWRREGGEASDKPIDSAYLSRMKQF 345
QY 455 LRATPKRLALKALSKALREDELVLYLKQFKLE-PRGFGSLNPNFALRLRYLTDAKE 513
DB 346 RAMNKLKMAKLVASNNNEEIKGLKMPNNMOTDNGSTIYELKAGLAK-LGSKLSE 404
QY 514 SRVLEFLHALPELAYRRMDEFEFCAAISPYLEALRMEIAGTARQOFEQGNRVISV 573
DB 405 AEVQUMEAADVNGSIDYVEFTATMHRKLER---DEHLFKARQYFDKNSGFTIR 460
QY 574 EEL-----AOELNLAPTHYSIVODMIRKSGKLNFLGFTFLNG 612
DB 461 DELESALIEHMGDTSTIRETISEVDTDNDGRINVEEFCAMRG 504

RESULT 5
ID CDPK_DAUCA STANDARD; PRT; 532 AA.
AC P28582;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALCIUM-DEPENDENT PROTEIN KINASE (EC 2.7.1.-) (CDPK).
OS Daucus carota (Carrot).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;
OC Asteridae: easterids II; Apiales: Apiaceae: Daucus.
OX NCBI_TaxID=4039;
RN [1]
RP SEQUENCE FROM N.A.
RA Choi J.H.;
RL Submitted (JAN-1997) to the EMBL/Genbank/DBD databases.
RN [2]
RP SEQUENCE OF 108-532 FROM N.A.
RX MEDLINE=92003674; PubMed=1912486;
RA Suen K.-L., Choi J.H.;
RT "Isolation and sequence analysis of a cDNA clone for a carrot
RT calcium-dependent protein kinase: homology to
RT calcium/calmodulin-dependent protein kinases and to calmodulin."
RL Plant Mol. Biol. 17:581-590(1991).
CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY
CC PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X56599; CAA39936.1; -
DR PIR: S17759; S17759.
DR HSSP: Q63450; 1A06.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk.pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.

DR Pfam: PF00036; ehand; 4.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM0054; Eph; 4.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00018; EF_HAND; 4.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR Transferrase: Serine/threonine-protein kinase; ATP-binding;
 KW Calcium-binding; Phosphorylation.
 FT DOMAIN 81 339 PROTEIN KINASE.
 FT NP_BIND 87 95 ATP (BY SIMILARITY).
 FT BINDING 110 110 ATP (BY SIMILARITY).
 FT ACT_SITE 205 205 BY SIMILARITY.
 FT CA_BIND 395 406 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 431 442 EF-HAND 2 (POTENTIAL).
 FT CA_BIND 465 476 EF-HAND 3 (POTENTIAL).
 FT CA_BIND 500 511 EF-HAND 4 (POTENTIAL).
 FT CA_BIND 511 511 EF-HAND 4 (POTENTIAL).
 SQ SEQUENCE 532 AA; 60065 MW; F03E6F036A0AE348 CRC64;

Query Match 26.0%; Score 847.5; DB 1; Length 532;
 Best Local Similarity 36.5%; Pred. No. 9,6e-38;
 Matches 201; Conservative 95; Mismatches 189; Indels 65; Gaps 14;

QY 95 RSTPRRRF-----KRPPPPSPAKHAKATLAKRLGGG-KRREGTIPPEGGVAG 142
 DB 18 RSPATVHYHYTDOSYKSSRSRQPOPOVOOT-----GSLAKRQVHRPSNTI--- 69
 QY 143 GGGGGAADGAEFRPLDKTFGFSKNFGAKYELKEVGRGHG--HTCSAVVKKGEYKGT 200
 DB 70 -----LGKPF-----EDIRKTYTLGKELGRGFGVCYCTE-----NSSGQL 106
 QY 201 VAVKIIRAKKMTAIEIDVRREVKKILRALSGNNINLYKFDACEDGQINVIYVWELCGGE 260
 DB 107 YAKSTLKRRLVSKNDEKEDIKREIQLDHLGSPNTVEEFQVEDROSVHLVWELCGGE 166
 QY 261 LLDRIARGRYTEEDAKAIVQILSVVAFCHLQGVVHRDLKPENFLFTTRDENAPMKLI 320
 DB 167 LFRITIAQ-GHYSERAAATICRQIVNVVHCHMGVHNRDLKPENFLSSKDDAMLKAT 225
 QY 321 DFGLSPIRDEFLNDIVGSAVYVAVBEVLRSTYSMEADWSIGVITYILLGSRPFWART 380
 DB 226 DEFGLSYFIEGKYYRNVIGSAVYVAVBEVLRSTYSMEADWSIGVITYILLGSRPFWAEN 285
 QY 381 ESGIFFSVLRADNPDPSPPTVSAEKDQVKKRFLNKDYKRMATAYALTHPMLRD--EQ 438
 DB 286 EKGFPAILEGVIDFSEPPSPVSNKDLVRKMLTQDPRRRTLSAQVLDHPMWRGGEA 345
 QY 439 RQIPDLIDFLRLIKOYLKATPLKRLALKALSKALREDELLYLKLOFKILE-PRDGEVSLD 497
 DB 346 SDKPIDSAVLSRKKOFRAKMKLQKALKVIAESISEEELIGLSMFANMDTDSGTTIYE 405
 QY 498 NFEATLTRYITDAMKESRYVEFLHLEPLAYRRMDFEEFCAAIISPYOLEALERMELIAG 557
 DB 406 ELKSGIAR-LGSKLSEVYQQLMDADVDNGTIDYLEFTTAMHRRKLSYSY----- 458
 QY 558 TAFQFQEGNRYISYEELAQELNL-----APTHYSIVQDMIRKSDGLNFGTKFLHG 612
 DB 459 QAFQYFDKDNISGFTTDELESAMKEYGMDEATIKDIISEVDSNDGRINYDEFCAAMR- 517
 QY 613 VTIRGSNTRR 622
 DB 518 ---RARRRR 524

RESULT 6
 CDPK_SOYBN STANDARD; PRT; 508 AA.
 ID CDPK_SOYBN
 AC P28583;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last annotation update)
 DT 20-AUG-2001 (Rel. 24, Last annotation update)

DE CALCIUM-DEPENDENT PROTEIN KINASE SK5 (EC 2.7.1.1) (CDPK).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, WILLIAMS;
 RX MEDLINE=91240279; PubMed=1852075;
 RA Harper J.F., Sussman M.R., Schaller G.E., Putnam-Evans C.,
 RA Chardonneau H., Harmon A.C.;
 RT "A calcium-dependent protein kinase with a regulatory domain similar
 to calmodulin";
 RL Science 252:951-954(1991).
 CC - FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
 INVOLVE CALCIUM AS A SECOND MESSENGER.
 CC - ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY
 PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
 CC - TISSUE SPECIFICITY: FOUND THROUGHOUT THE PLANT.
 CC - MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN SOYBEAN.
 CC - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC - SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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 or send an email to license@sib-sib.ch).
 CC EMBL: M64987; AAB00806.1; -
 CC PIR: A43713; A43713.
 CC DR HSSP: Q63450; 1A06.
 CC DR InterPro: IPR002048; EF-hand.
 CC DR InterPro: IPR000719; Euk_pkinase.
 CC DR InterPro: IPR002290; Ser_thr_kin_actsite.
 CC Pfam: PF00036; ehand; 4.
 CC Pfam: PF00069; pkinase; 1.
 CC SMART: SM00054; Eph; 4.
 CC SMART: SM00220; S_TKc; 1.
 CC PROSITE: PS00018; EF_HAND; 4.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 CC Transferrase: Serine/threonine-protein kinase; ATP-binding;
 KW Calcium-binding; Phosphorylation.
 FT DOMAIN 34 292 PROTEIN KINASE.
 FT NP_BIND 40 48 ATP (BY SIMILARITY).
 FT BINDING 63 63 ATP (BY SIMILARITY).
 FT ACT_SITE 158 158 BY SIMILARITY.
 FT CA_BIND 348 359 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 384 395 EF-HAND 2 (POTENTIAL).
 FT CA_BIND 420 431 EF-HAND 3 (POTENTIAL).
 FT CA_BIND 454 465 EF-HAND 4 (POTENTIAL).
 SQ SEQUENCE 508 AA; 57169 MW; AFCEDC51224192E4 CRC64;

Query Match 25.1%; Score 817; DB 1; Length 508;
 Best Local Similarity 38.9%; Pred. No. 3,6e-36;
 Matches 178; Conservative 94; Mismatches 160; Indels 26; Gaps 11;

QY 165 SKNGAKYELCKEYGRGHGHT--CSAVVKKGEKGTAVAKIIRAKKMTAISIEVRR 222
 DB 27 TQNIREFYEWGRKLGQGFTECTRRASGKF-----ACKSLPKRKLCKEDYEDVWR 81
 QY 223 EVKILRALSGNNLVKRYDACEEDGLANYIYVWELCGEGLDRIARGRYTEEDAKAIVV 282
 DB 82 EIQIMHLSSEHANYVRLEGTEEDSTAVHLVWELCGEGELPRIVYQK-GHYSERAAALIK 140
 QY 283 QILSVAFCHLQGVVHRDLKPENFLFTTRDENAPMKLIDFGLSDFIRPDERLNDIVGSAY 342

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Db 141 TIVEVEACHSLGVWHRDLKPFENLFDIDEDAKLAKTDGLSLFYFPGSGFCDVGSPPY 200
Oy 343 YVAPEVLRHSYMSMADWISIVITITLLCGSRPFWANTSGIFRSVLADPNFDDSPWPT 402
Db 201 YVAPEVLKLLGPPSDWASAGVITLLSGVPFWASESGIFRQILLGLKDFHSEFWPS 260
Oy 403 VSAEAKDFVKKRFLNKDYRKRTAVOALTHPMLRDEQ--RQIPDILIFRIKYLATPL 460
Db 261 ISDSAKDLIRKMLDQNKRTLRTHAEVLRHWIYDDNAPRKLDSAVLSRLKQPSAMNKL 320
Oy 461 KRLAKLAKSRKREDELLYLKLOFLE--PRDGFVSLDNRTALTRYLTDAMKESVLEF 519
Db 321 KKMALRYAERLSEELGKRELFKMDTNSGTFTEDELKDKLRVGSFLM--ESSEIKDL 379
Oy 520 LHALEPLAYRRMDFEECAAIISPYOLEALRMEELIAGTAFQFQEDGKRVISVELAQ- 578
Db 380 MDADADIKSGTIDYGEFIATV---HLNKLREELNV-SAFSYFDKDGSGYITLDEIQQA 435
Oy 579 --ELNLAPTHYSIVQDMIRK---SDGKLNFLGTFKL 610
Db 436 CKDFGLDDIH---IDMKIRIIDDNDGQIDYGEFAMM 470

```

RESULT 7

CDP3_ORYSA STANDARD: PRT; 542 AA.

```

AC P53684;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALCULUM-DEPENDENT PROTEIN KINASE, ISOFORM 11 (EC 2.7.1.-) (CDPK 11).
GN CPK11.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ARBORIO; TISSUE=coleoptile;
RA MEDLINE=95284352; PubMed=7766885;
RA Breviarlo D., Morello L., Giant S.;
RT "Molecular cloning of two novel rice cDNA sequences encoding putative
RT calcium-dependent protein kinases."
RL Plant Mol. Biol. 27:953-967(1995).
CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC -1- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CANK SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS. THREE OF
CC THEM SEEM TO BE NON FUNCTIONAL.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR HSP: X81393; CAA57156.1; -
DR HSP: O63450; JAO6.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk_pkinase.
DR Pfam: PF00036; ehand; 4.
DR Pfam: PF00069; kkinase; 1.
DR SMART: SM00054; EKH; 3.
DR SMART: SM00220; S_LNC; 1.
DR PROSITE: PS00018; EF_HAND; 1.

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DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation; Multisite family.
FT DOMAIN 79 337 PROTEIN KINASE.
FT NP_BIND 81 89 ATP (BY SIMILARITY).
FT BINDING 107 107 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
FT DOMAIN 393 404 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 429 440 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT DOMAIN 465 476 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
FT CA_BIND 499 510 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 542 AA; 6116 MW; D4D257275C126DDA CRC64;

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Query Match 24.4%; Score 794; DB 1; Length 542;

Best Local Similarity 34.6%; Pred. No. 6.2e-35;

Matches 185; Conservaive 101; Mismatches 189; Indels 60; Gaps 13;

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Oy 125 GAKREGIT-----PEEGVGAGGGGGGADGAETFRPLDTFGFSKFN----- 168
Db 2 GNOCNGTIGSDYHNRRPREHAGVYOG-----DSYLDKKFDPTWPEVNNFKPTASTL 56
Oy 169 -----GAK-----YELGKEVGRGHGHT--CSAYVKKGEYAGQTVAAKI 207
Db 57 RRGIDPTISINVLGKRTYDLREHYITIGKLGQAFGTYITCTEINTGCEY-----ACKTIP 111
Oy 208 KAKMTAISIEDVREVKILRALSGHNLVKFADCEGLNVTYVMELEGSELRLRLA 267
Db 112 KRLITLEDVEDVAREIQIHNLHLSGKNVVAINDYEDGQAVIIVELCAGGLPRIDR 171
Oy 268 RGGVTEEDAKIYVOLLVYVACHLQGVVHRDLKPNLEFTRDENAPKLLIDFGLSDP 327
Db 172 K-GHYSERRKAELRIIVSIVAMCHSLGVWHRDLKPFENLFDIDEDAKLAKTDGLSL 230
Oy 328 IRPDERLNDIVGSAYYAPVLRHSYMSMADWISIVITITLLCGSRPFWANTSGIFRS 387
Db 231 FKRGQVTELVGSPYYAPRVLRKRGPESDVWASAGVITLLSGVPFWAETQGSIFDA 290
Oy 388 VLRADPNFDDSPWTVSAEAKDFVKKRFLNKDYRKRTAVOALTHPMLRDE--RQIPDIL 445
Db 291 VLGKIHDFQSDPWPWKISDSAKDLIRKMLSHCPSERLKANEVLRHWICNGVATQADLP 350
Oy 446 LIFRLIKOYLRATPLRKLALSKALREDELLYLKLOFLEPRD--GFVSLDNRTALT 504
Db 351 SVTSRLKQPSAMNKLKRLALRYAERLSEELAGLEMEKAVDTKNRGVITFGELREGIR 410
Oy 505 RYLTDMKESRYLEFLHALEPLAYRRMDFEECAAIISPYOLEALRMEELIAGTAFQFQ 564
Db 411 RFGEAE-FKDTIELGIDMEAHNNNNVTIHYEFRIATL---PLNKIEREHL-ANFTYFD 465
Oy 565 QEGNRYISVELAEOLNLAPTHYSIVQDMI---RKSDGKLNFLGTFKLHGVTI 615
Db 466 KDSGGYITVDKLORACGEHNMEDSLLEIISVDNDNDGQIDYAEFVAMQGSNV 520

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RESULT 8

CDP1_ORYSA STANDARD: PRT; 534 AA.

```

AC P53682;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALCULUM-DEPENDENT PROTEIN KINASE, ISOFORM 1 (EC 2.7.1.-) (CDPK 1).
GN SPK.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;

```


RX MEDLINE-93314961; PubMed-8325505;
 RA Kawasaki T., Hayashida N., Baba T., Shinozaki K., Shimada H.;
 RT "The gene encoding a calcium-dependent protein kinase located near
 the shb1 gene encoding starch branching enzyme I is specifically
 expressed in developing rice seeds."
 RL Gene 129:183-189(1993).
 CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
 CC INVOLVE CALCIUM AS A SECOND MESSENGER.
 CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
 CC -1- DEVELOPMENTAL STAGE: SPECIFICALLY EXPRESSED IN SEEDS.
 CC -1- MISCELLANEOUS: THERE ARE MULTIPLE CDK ISOFORMS IN RICE.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS. THREE OF
 CC THEM SEEM TO BE NON FUNCTIONAL.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: D13436; BAA02698.1; -
 CC HSSP: P02593; 1CDM.
 CC InterPro: IPR002048; EF-hand.
 CC InterPro: IPR000719; Euk.pkinase.
 CC InterPro: IPR002290; Ser_thr_kin_actsite.
 CC Pfam: PF00036; efhand; 4.
 CC Pfam: PF00069; pkinase; 1.
 CC SMART: SM0054; EFh; 2.
 CC SMART: SM00220; S_TKc; 1.
 CC PROSITE: PS00018; EF_HAND; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
 CC Calcium-binding; Phosphorylation; Multigene family.
 CC FT DOMAIN 73 331
 CC NP_BIND 79 87
 CC BINDING 102 102
 CC ACT_SITE 197 197
 CC DOMAIN 387 398
 CC DOMAIN 422 432
 CC DOMAIN 457 468
 CC CA_BIND 491 502
 CC SEQUENCE 534 AA: 60573 MW: 19320204.85 FC64;
 CC
 CC Query Match 22.9%; Score 747; DB 1; Length 534;
 CC Best local similarity 36.4%; Pred. No. 1.8e-32;
 CC Matches 176; Conservative 93; Mismatches 184; Indels 30; Gaps 13;
 CC
 CC 146 GGAAGAETPRDKTGF- SKNFGAYELGKEVGRGHFT--CSAVVKKGEYGTVA 202
 CC 49 GALRQGLNLSKSPV---LGYKTPVRYELTGLRGELGQGFQKTYLCTEISTSGCQ-----A 100
 CC
 CC 203 VKIIAKAKMTTALSIEDEYREVKKILRLSGHNNLYKYDACEGLNYYIWEACEGELL 262
 CC 101 CKTILSNLNCVSDIEDEYREIOMHLSGOKNVTIKDYDEQAVHAIWEACAGGELL 160
 CC 263 DRIIARGRTEDAKAIVQILSVAFCHLOGVHRDLPENFLPTTRBNAPMKLIDF 322
 CC 161 SKIQKR-GHYSERKAELIITVIGITCSHGVMHDLKPENFLLDADDESVKAIIDF 219
 CC 323 GLSDFTNRLNDIVGSAVYVAPELHRSYSMEADTWSIGVITYILLGSSRPFWARTES 382
 CC 220 GLSVFRPGGVFREVGSPPYIAPEVLEKRYGPEADITWAGVILYVLTGVPFWADTQS 279
 CC 383 GTRSVYLRADPNDDSWPVPYSAKDFVYKFLNKKYRKRTAVQALTHWLRDE--QRO 440
 CC 280 GIYEKVLDRIDKSNRMPRISDASKDLIKMLCPYPLERLKAHEVLKHPMICNGVATN 339

QY 441 IPIDLIFRLIKOYLKATPLKRLALKSKALREDELLYKLOFKLEPRDGEVSLDNFR 500
 DB 340 RALDPSVLRPLKQFSANNRLKKSIOIARLSSEELVGRBEMKANDTNRSVYTFGEL 399
 QY 501 TALTRYITDMKESRVLFEFLHLEPLAYRMDPEECFAAISPYOLEALEREIECTAF 560
 DB 400 KGKRYR-SYVEKDEITINDLEADDDT-STINMEEFYAAVS--LNKIER-EKHMAAF 453
 QY 561 QOFEOENRIVSVEEL--AOELNLAPTH-STYODMIRKSDKLNPLGFTKFLHGYTIR 616
 DB 454 TYFDKDSGFTYVDKLOKACMERMEDTLEEMILEVDONNDGIDYAEF-----VTMM 507
 QY 617 GSN 619
 DB 508 QSN 510
 CC
 CC RESULT 9
 CC KCCL_HUMAN STANDARD; PRT; 370 AA.
 CC ID KCCL_HUMAN
 CC AC 014012:
 CC DT 15-JUL-1998 (Rel. 36, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
 CC DT 20-AUG-2001 (Rel. 40, Last annotation update)
 CC DE CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123)
 CC DE (CAM KINASE I).
 CC GN CAMK1.
 CC OS Homo sapiens (human).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 CC OX NCBI_Taxid:9606;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE-95369239; PubMed-7641687;
 CC RA Haribabu B., Hook S.S., Selbert M.A., Goldstein E.G., Tomhave E.D.,
 CC Ebelman A.M., Snyderman R., Means A.R.;
 CC RT "Human calcium-calmodulin dependent protein kinase I: CDNA cloning,
 CC domain structure and activation by phosphorylation at threonine-177
 CC by calcium-calmodulin dependent protein kinase I kinase."
 CC RL EMBO J. 14:3679-3686(1995).
 CC
 CC -1- FUNCTION: PHOSPHORYLATES SYNAPSTIN I.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN -> ADP + A PHOSPHOPROTEIN.
 CC -1- ENZYME REGULATION: ACTIVATED BY CA++/CALMODULIN. MUST BE
 CC PHOSPHORYLATED TO BE MAXIMALLY ACTIVE.
 CC -1- SUBUNIT: MONOMER.
 CC -1- TISSUE SPECIFICITY: UBQUITOUS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: L41816; AAA99458.1; -
 CC HSSP: Q63450; 1A06.
 CC KIM; 604998.
 CC InterPro: IPR000719; Euk.pkinase.
 CC InterPro: IPR002290; Ser_thr_kin_actsite.
 CC Pfam: PF00069; pkinase; 1.
 CC SMART: SM00220; S_TKc; 1.
 CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 CC PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
 CC Transferrase; Serine/threonine-protein kinase; Calmodulin-binding;
 CC Phosphorylation; ATP-binding; Alternative splicing.
 CC FT DOMAIN 20 276
 CC NP_BIND 287 321
 CC SEQUENCE 26 34
 CC CALMODULIN-BINDING (BY SIMILARITY).
 CC ATP (BY SIMILARITY).

GN CAMK4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SYKAIN-BALB/C; TISSUE=Brain;
 RA MEDLINE=91372388; PubMed=1893997;
 RA Jones D.A., Glod J., Wilson-Shaw D., Hahn W.E., Sikela J.M.;
 RT "cDNA sequence and differential expression of the mouse
 RT Ca2+/calmodulin-dependent protein kinase IV gene.";
 RL FEBS Lett. 289:105-109(1991).
 RN [2]
 RP SEQUENCE OF 240-469 FROM N.A.
 RX MEDLINE=89122027; PubMed=2536634;
 RA Sikela J.M., Law M.L., Kao F.-T., Hartz J.A., Wei Q., Hahn W.E.;
 RT "Chromosomal localization of the human gene for brain
 RT Ca2+/calmodulin-dependent protein kinase type IV.";
 RL Genomics 4:21-27(1989).
 RN [3]
 RP SEQUENCE OF 315-469 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=87204263; PubMed=3033675;
 RA Sikela J.M., Hahn W.E.;
 RT "Screening an expression library with a ligand probe: isolation and
 RT sequence of a cDNA corresponding to a brain calmodulin-binding
 RT protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3038-3042(1987).
 CC -1- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
 CC PROTEIN.
 CC -1- CATALYTIC ACTIVITY: ATP + PROTEIN = ADP + O-PHOSPHOPROTEIN.
 CC -1- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
 CC NUCLEI.
 CC -1- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
 CC TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: BRAIN AND TESTIS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: M6206; AAA39933.1; -;
 DR EMBL: M64266; AAA37364.1; -;
 DR EMBL: J03057; AAA37366.1; -;
 DR EMBL: X58995; CAA41741.1; -;
 DR PIR: A29878; A29878.
 DR PIR: S17656; S17656.
 DR HSSP: O63450; 1A06.
 DR MGD: MGI:88258; Camk4.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR Pfam: PF00069; S_krc; 1.
 DR SMART: SM00220; S_krc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
 KM Transfease; Serine/threonine-protein kinase; ATP-binding;
 KW Calmodulin-binding; Alternative splicing.
 FT CHAIN 306 469
 FT DOMAIN 42 296
 FT NP_BIND 48 56
 FT BINDING 71 71
 FT ACT_SITE 160 160
 FT DOMAIN 318 337
 FT CONFLICT 278 280
 VLD -> CPGI (IN REF. 2).

FT CONFLICT 302 302 N -> T (IN REF. 2).
 SQ SEQUENCE 469 AA; 52627 MW; CEIF98670822F975 CRC64;
 Query Match 15.4%; Score 501; DB 1; Length 469;
 Best Local Similarity 35.9%; Pred. NO. 1.1e-19;
 Matches 120; Conservative 57; Mismatches 109; Indels 48; Gaps 11;
 QY 105 PFPSPSPAKHIKATLAKRLGGKPKREKTIPEEGVGAGGGGGAADGAETERPDKTFGF 164
 DB 7 PSCSPSSCVSTAS-----TENLVDPDY-----IDSNND-PL----- 38
 QY 165 SKNFGAKYELKEVGRGHFGHTCSAVVKKGEKG--QTVAKIITAKKMTAISIEDVRR 222
 DB 39 -----GDFEEVESSELGRG-----ATSIYRCOKQKQTPKPYALKVLK-----TVDKKIVRT 84
 QY 223 EVKILRLASGNNLVKRYDACCEDGLNYYIWECEGSELLDRILARGRYTEEPKAIIV 282
 DB 85 EIGVLLRLS-HPNILIKELFETPTESLVELVTGGELEDRIVEK-GYTSERDARAVK 142
 QY 283 QILSVAFCHLGGVHRDLKRENFLETTDENAPMKLIDFGLSDPIRDERLANDVGSAY 342
 DB 143 QILEAVAVLHENGIVHRDLKRENLLYATPADAPKLTADRLSKIVEROVLMKTCGTPG 202
 QY 343 YVAPVLRH-SYSEADIWISGIVTYILLGSRPFW-ARTESGIFRSVLRADPNFDDSPW 400
 DB 203 YCAPEIIRGCAYGPEVDMWSGIIITYILLGCEFFPERGCDQFMFRILNCEYFISPMW 262
 QY 401 PTVASPAKDPYKRLNDRKRYKMTAVOALTHPWL 434
 DB 263 DEVSLNMDLVKLLVDPKRLITFQALQHPWV 236
 RESULT 12
 KMLC_DICDI
 ID KMLC_DICDI STANDARD; PRT; 295 AA.
 AC P25323;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).
 GN MKA.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX3;
 RX MEDLINE=91340753; PubMed=1651931;
 RA Tan J.L., Spudich J.A.;
 RT "Characterization and bacterial expression of the Dictyostelium
 RT myosin light chain kinase cDNA. Identification of an autoinhibitory
 RT domain.";
 RL J. Biol. Chem. 266:16044-16049(1991).
 RN [2]
 RP REVISIONS.
 RA Spudich J.A.;
 RL Submitted (AUG-1996) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP PARTIAL SEQUENCE.
 RC STRAIN=AX3;
 RX MEDLINE=90337997; PubMed=2380188;
 RA Tan J.L., Spudich J.A.;
 RT "Dictyostelium myosin light chain kinase. Purification and
 RT characterization.";
 RL J. Biol. Chem. 265:13818-13824(1990).
 CC -1- FUNCTION: PHOSPHORYLATES A SPECIFIC SERINE IN THE N-TERMINUS OF A
 CC MYOSIN LIGHT CHAIN.
 CC -1- CATALYTIC ACTIVITY: ATP + [MYOSIN LIGHT-CHAIN] = ADP + [MYOSIN
 CC LIGHT-CHAIN] PHOSPHATE.
 CC -1- ENZYME REGULATION: POSSESSES AN AUTOINHIBITORY DOMAIN.
 CC AUTOPHOSPHORYLATION APPEARS TO INCREASE THE ENZYMATIC ACTIVITY.
 CC DOES NOT HAVE A CALMODULIN-BINDING DOMAIN.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: M66176; AB06337.1; -
 DR PIR: A40811; A40811.
 DR PIR: A37125; A37125.
 DR HSSP: Q63450; 1A06.
 DR Dictydb: DD01034; mlka.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW phosphorylation.
 FT DOMAIN 8 265 PROTEIN KINASE.
 FT NP_BIND 264 295 AUTONINIBITORY DOMAIN.
 FT BINDING 14 22 ATP (BY SIMILARITY).
 FT ACT_SITE 37 37 ATP (BY SIMILARITY).
 FT ACT_SITE 130 130 BY SIMILARITY.
 SQ SEQUENCE 295 AA; 33406 MW; 546CAED8F6ECD0B CRC64;

Query Match 15.3%; Score 498; DB 1; Length 295;
 Best Local Similarity 38.7%; Pred. No. 9.7e-20;
 Matches 111; Conservative 57; Mismatches 103; Indels 14; Gaps 7;

QY 172 YELGKGVGRGHGHTGSAVYKGGYK--GGTVAVKIIAKAKMTAISIEDVRRREVKILRA 229
 DB 8 YEFKEEELGRGAF-----SIYVLGENKQTKORVAIKYINKSELGDYE-KMLKMEVDILK 61

QY 230 LSGNNLVKRYDACEGDLNVIYMEICEGSELLDRILARSGRTTEDEAKAIYVQILSYVA 289
 DB 62 VN-HPNIIALKEFDPEKIKYLMELTGGELDKIVKESG-YSEDAANLVKRIYSAVG 119

QY 290 FCHLQGVVHDLKPENFLFTTRDENAPMKLIDFGLSDFIRPDERLNDIYGSAYVAPEVL 349
 DB 120 YLHGLNIVHDLKPENFLFTTRDENAPMKLIDFGLSDFIRPDERLNDIYGSAYVAPEVL 179

QY 350 HRS-YSEADINSIGVITTYILLGSGRPFARTEGIFRSVLRADPNEDDSFMPPTVSAEAK 408
 DB 180 NATGYDEKVDMSIGVITTYILLGSGRPFARTEGIFRSVLRADPNEDDSFMPPTVSAEAK 239

QY 409 DFKVRFLEKNDYRKRTAVQALTRPMLDEQRQIPLDILFRLKOYL 455
 DB 240 DFLGKLLVYDVSKRLNATNALNHPMLKSNNSNTIDTV--KKKEYI 283

RESULT 13
 KC4_RAT
 ID KC4_RAT STANDARD; PRT; 474 AA.
 AC P13234;
 DT 01-JAN-1990 (rel. 13, Created)
 DT 01-APR-1993 (rel. 25, Last sequence update)
 DT 20-APR-2001 (rel. 40, Last annotation update)
 DE CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN
 DE (EC 2.7.11.23) (CAM KINASE-GR) (CAMK IV) [CONTAINS: CALSPERMIN].
 GN CAMK4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE-91288548; PubMed-1648230;
 RA Oimstede C.-A., Bland M.M., Merrill B.M., Sahyoun N.;
 RT "Relationship of genes encoding Ca2+/calmodulin-dependent protein
 RT kinase Gr and calsperrin: a gene within a gene."
 RT Proc. Natl. Acad. Sci. U.S.A. 88:5784-5788(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-91304387; PubMed-1649385;
 RA Means A.R., Cruzalegui F., Lemagueresse B., Needleman D.S.,
 RA Slaughter G.R., Ono T.;
 RT "A novel Ca2+/calmodulin-dependent protein kinase and a male germ
 RT cell-specific calmodulin-binding protein are derived from the same
 RT gene."
 RT Mol. Cell. Biol. 11:3960-3971(1991).
 RN [3]
 RP SEQUENCE OF 250-474 FROM N.A.
 RC STRAIN-SPRAGUE-DAMLEY; TISSUE-Brain;
 RX MEDLINE-89174647; PubMed-2538431;
 RA Oimstede C.-A., Jensen K.F., Sahyoun N.;
 RT "Ca2+/calmodulin-dependent protein kinase enriched in cerebellar
 RT granule cells. Identification of a novel neuronal
 RT calmodulin-dependent protein kinase."
 RT J. Biol. Chem. 264:5866-5875(1989).
 RN [4]
 RP SEQUENCE OF 306-474 FROM N.A., AND SEQUENCE OF 335-361.
 RC STRAIN-SPRAGUE-DAMLEY;
 RX MEDLINE-89123272; PubMed-2914893;
 RA Ono T., Slaughter G.R., Cook R.G., Means A.R.;
 RT "Molecular cloning sequence and distribution of rat calsperrin, a
 RT high affinity calmodulin-binding protein."
 RT J. Biol. Chem. 264:2081-2087(1989).
 RL [1]
 CC -1- FUNCTION: CAM KINASE GR IS A NEURONAL-SPECIFIC PROTEIN KINASE,
 CC ENRICHED IN CEREBELLAR GRANULE CELLS.
 CC -1- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
 CC PROTEIN.
 CC -1- CATALYTIC ACTIVITY: ATP + PROTEIN - ADP + O-PHOSPHOPROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
 CC TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: CALSPERMIN IS PREDOMINANTLY FOUND IN MAMMALIAN
 CC TESTIS AND BRAIN.
 CC -1- PTM: THE N-TERMINAL OF CALSPERMIN IS BLOCKED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M63334; AAA40865.1; -
 DR EMBL: M74488; AAA40845.1; ALT_SEQ.
 DR EMBL: M64757; AAA40856.1; -
 DR EMBL: M64757; AAA40857.1; -
 DR EMBL: J04600; AAA41867.1; -
 DR EMBL: J04446; AAA40990.1; -
 DR PIR: A41103; TVRICA.
 DR HSSP: Q63450; 1A06.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
 KW Calmodulin-binding; Testis; Alternative splicing.
 FT CHAIN 306 474 CALSPERMIN.
 FT DOMAIN 42 296 PROTEIN KINASE.

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FT NP_BIND 48 56 ATP (BY SIMILARITY).
FT BINDING 71 71 ATP (BY SIMILARITY).
FT ACT_SITE 160 160 CALMODULIN-BINDING (POTENTIAL).
FT DOMAIN 318 337 POLY-GLU.
FT DOMAIN 393 399 POLY-GLU.
FT DOMAIN 403 413 POLY-GLU.
FT CONFLICT 372 372 I -> M (IN REF. 2 AND 4);
SQ SEQUENCE 474 AA; 53133 MW; 56F71AC5644DED23 CRC64;

Query Match 15.2%; Score 495; DB 1; Length 474;
Best Local Similarity 35.6%; Pred. No. 2.4e-19;
Matches 119; Conservative 57; Mismatches 110; Indels 48; Gaps 11;

OY 105 PPPSPAHKATLAKRLGGCKPKEGTPEEGVGAGGGGCAACGAEPRDLTKTFCF 164
DB 7 PSCPSSPCSSVSS-----TENLVPDV-----IDGSKRD-PLSPFF-- 42
OY 165 SKNFGAKYELGKRGHGHGHTCSAVVKKGEYKG--QTVAVKLIAMAKMTAISIEDVR 222
DB 43 -----EVESLGRG-----ATSIYRCOKGQTKPKALKVKK-----TVDKKIVRT 84
OY 223 EKKILALSGHNNLVKFTYACEDGLNVYVMECEGELLRLANGRTEDAKAIYV 282
DB 85 EGVGLRLS-HPNITLKEIFETPTETISLVLELVGCELFDRIVERK-GVYSERDADAVK 142
OY 283 QILSVAFCHLOGVVRDLKPENFLFTRDENAPMKLIDFGSLDFIRPERLNDIVGSAY 342
DB 143 QILEAVAYIHENGIYHRDLKPENLATAPADPKLIADGSKIVYEHQVLMKTVCGTFC 202
OY 343 YVAEVLNR-SYSMEADINSIGVITYILLGSRHFV-ARTESGIFRSVLADPNFDSFP 400
DB 203 YCAPELRBCAAGPEVDMMVSGIITYILLGCFEPFYDEKGDQMFRIINCEYFISPMW 262
OY 401 PIVSAPAKPFVKFLNKDYRKMTAVOALTHPVL 434
DB 263 DEVSLNAKDLVKKLIIVLDPKRLTTFQALQHPV 296

RESULT 14
KCC1_YEAST STANDARD; PRT; 446 AA.
ID KCC1_YEAST PRT; 446 AA.
AC P27466;
DC 01-AUG-1992 (Rel. 23, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE I (EC 2.7.1.123).
GN CMK1 OR YER014C.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxId=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-91224102; PubMed-2026147;
RA Pausch M.H., Kaim D., Kunisawa R., Admon A., Thorner J.;
RT "Multiple Ca2+/calmodulin-dependent protein kinase genes in a
uniceellular eukaryote.";
RL EMBO J. 10:1511-1522(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-91286319; PubMed-2061341;
RA Ohya Y., Kawasaki H., Suzuki K., Londesborough J., Anraku Y.;
RT "Two yeast genes encoding calmodulin-dependent protein kinases.
Isolation, sequencing and bacterial expressions of CMK1 and CMK2.";
RL J. Biol. Chem. 266:12784-12794(1991).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RA MEDLINE-95400292; PubMed-7670463;
RA Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M.,
Sasakuma S.-I., Sasakuma M., Tsuchiya Y., Soeda E., Yokoyama K.,
Yamazaki M., Tashiro H., Eki T.;

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RT RT
RT Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae.";
RL Nat. Genet. 10:268(1995).
CC -I- FUNCTION: IMPORTANT IN CELLULAR REGULATION.
CC -I- CATALYTIC ACTIVITY: ATP + A PROTEIN -> ADP + A PHOSPHOPROTEIN.
CC -I- SUBUNIT: MULTIMERIC.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CMK SUBFAMILY.
CC -----
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CC or send an email to license@isb-slb.ch).
CC -----
DR EMBL: X57782; CAA0928.1; -
DR EMBL: D90375; BAA14383.1; -
DR EMBL: D50617; BAA09253.1; -
DR EMBL: D44599; BAA08031.1; -
DR PIR: A40896; A40896.
DR PIR: S16883; S16883.
DR HSSP: Q63450; 1A06.
DR SGD: S0001910; CMK1.
DR InterPro: IPR000719; Euk_kinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase: Serine/threonine-protein kinase; Calmodulin-binding;
KW Phosphorylation; ATP-binding; Multigene family.
FT DOMAIN 37 299
FT NP_BIND 43 51 ATP (BY SIMILARITY).
FT BINDING 66 66 ATP (BY SIMILARITY).
FT ACT_SITE 161 161 CALMODULIN-BINDING (BY SIMILARITY).
FT DOMAIN 312 323
FT CONFLICT 53 54 OA -> VR (IN REF. 1).
FT CONFLICT 68 68 L -> V (IN REF. 1).
FT CONFLICT 188 188 R -> T (IN REF. 1).
FT CONFLICT 199 202 PAGES -> AGTA (IN REF. 1).
FT CONFLICT 237 243 SAFRAER -> ATIDRK (IN REF. 1).
FT CONFLICT 271 271 K -> Q (IN REF. 1).
SQ SEQUENCE 446 AA; 50296 MW; 586C31CED6311555 CRC64;

Query Match 15.1%; Score 493.5; DB 1; Length 446;
Best Local Similarity 37.6%; Pred. No. 2.6e-19;
Matches 135; Conservative 46; Mismatches 123; Indels 55; Gaps 11;

OY 171 KYELGKEVGRGHGHTCSAVV--KGEYKQTYAVAKI-IKAKMTAISIEDVREYKIL 227
DB 36 KYVEGKTLGAGTGG-----VVRQAKNTGDEDAVAKILIKKAKGNKYOLEALYDELDIL 90
OY 228 RALSGHNNLVKFTYACEDGLNVYVMECEGELLRLANGRTYEDAKAIYOVLIS 287
DB 91 QRLH-HPNIVAFKDFESKSKFYITQLAKGELFDRILKK-GKTFEDAVRLIVELISA 148
OY 288 VAFCHLOGVVRDLKPENFLFTRDENAPMKLIDFGSLDFIRPER-LNDIVGSAYVAP 346
DB 149 VKVMHSGNIVYHRDLKPENLITIDKSDSPLVVADFGIARLKSDELLYKPAAGSLGVAP 208
OY 347 EVLNR-SYSMEADINSIGVITYILLGSRHFV-RTESGIFRSVLADP-NFDSFPPTY 403
DB 209 EVLTDGCHGRPCDIWSIGVITYILLGYSAFRAERVODFLDECTGTGEPVFRHPWDSV 268
OY 404 SAKAPKPFVKFLNKDYRKMTAVOALTHPVL-----RDEQR 439
DB 269 SKNAKQFIKALNLDPSKRTAAELLEDPIWICTELKTHNLGLKGLDAROKFRNSVE 328
OY 440 QIPDLILIFRLIKOYLRLAT-----PLKRLALALSKALREDELLYLK 481

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Db      329 RVLNKKIKLRLDYLEQTESDSDFDGSGANGSVPLKATDTLSKSLSEEGSKLK 387
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RESULT 15
KCC4_HUMAN STANDARD: PRT; 473 AA.
AC 016566;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE IV CATALYTIC CHAIN
DE (EC 2.7.1.123) [CAM KINASE-GR] [CONTAINS: CALSPERMIN].
CN CAMK4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=94375404; PubMed=8089075;
RA Kikani T., Okuno S., Fujisawa H.;
RT "cDNA cloning and expression of human calmodulin-dependent protein
RT kinase IV."
RL J. Biochem. 115:637-640(1994).
RN 12
RP SEQUENCE FROM N.A.
RX TISSUE=Cerebellum, and Thymus;
RX MEDLINE=94252566; PubMed=8194751;
RA Bland M.M., Monroe R.S., Ohmsted C.A.;
RT "The cDNA sequence and characterization of the
RT Ca2+/calmodulin-dependent protein kinase-Gr from human brain and
RT thymus."
RL Gene 142:191-197(1994).
RN 13
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RX MEDLINE=94149862; PubMed=8107230;
RA Mosllos G., Hanissian S.H., Jawahar S., Vara L., Kleff E.,
RA Chaitia T.A.;
RT "A Ca2+/calmodulin-dependent protein kinase, Cam kinase-Gr, expressed
RT after transformation of primary human B lymphocytes by Epstein-Barr
RT virus (EBV) is induced by the EBV oncogene LMP1."
RL J. Virol. 68:1697-1705(1994).
RN 14
RP FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
RP PROTEIN.
CC -1- CATALYTIC ACTIVITY: ATP + PROTEIN = ADP + O-PHOSPHOPROTEIN.
CC -1- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
CC NUCLEI (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE
CC TYPE IV CATALYTIC CHAIN AND CALSPERMIN ARE OBTAINED BY ALTERNATIVE
CC SPLICING.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
-----
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DR EMBL: D30742; BAA06403.1;
DR EMBL: L17000; AAA35639.1;
DR EMBL: U24959; AAA18251.1;
DR HSSP: Q63450; 1A06.
DR MIM: 114080;
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR003290; Ser_thr_kin_actsite.
DR Pfam: PF00069; Pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

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DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Calmodulin-binding; Alternative splicing.
FT CHAIN 310 473
FT DOMAIN 46 300 CALSPERMIN.
FT NP_BIND 52 60 ATP (BY SIMILARITY).
FT BINDING 75 75 ATP (BY SIMILARITY).
FT ACT_SITE 164 164 BY SIMILARITY.
FT DOMAIN 322 341 CALMODULIN-BINDING (POTENTIAL).
SQ SEQUENCE 473 AA; 51925 MW; EFEE515612326DC CRC64;

Query Match 15.0%; Score 490; DB 1; Length 473;
Best Local Similarity 40.1%; Pred. No. 4.3e-19;
Matches 107; Conservative 51; Mismatches 93; Indels 16; Gaps 7;

QY 172 YELGKEVGRGHFGHTGSAVVKKGKRYG--QTVAVKIIAKAKMTAISIEYRREVKILRA 229
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 46 FEVESELRG-----ATSIYRKOKGTOKPVALKVKR---TVDKKIVRTIEIGVLR 95
QY 230 LSGHNNLVKPYDACEGLNVIYIMELCEGELLDRILARGRYTEBDAAKAIYQILSYVA 289
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 96 LS-HPNIIKKKEIFETPTETISLVLEVTGGELEFDRIEYK-GYSESDADAVKQILLENVA 153
QY 290 FCHLOGVYHRDLKPEMFLPTTRDENAPMKLIDGSLDFTRPDERLNDIVGSAVYVAPEVL 349
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 154 YLENGIVHRDLKPEMFLVATPAPAPLAIADGSLKIEYHOVLKMTVCGTGYCAPELL 213
QY 350 HR-SYMEADIMSIGVITVILLGSRPFV-ARTESGIFRSVLRADNPFDSMPVYSAAE 407
      ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 214 RCGAYGPEYDMSVGIITVILLGFEPEFDERKDQMFRIINCEYFISPMWDEVSLNA 273
QY 408 KDFVKKFLNKDKRKRMTAVQALTHPWL 434
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 274 KDLVRLIYLDPRKRLITFQALQHPWV 300

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Search completed: May 2, 2002, 08:49:46
Job time: 565 sec

Thu May 2 11:46:28 2002

us-09-854-731-4.rsp

Page 13

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2002, 08:37:31 ; Search time 122.34 Seconds
(without alignments)
744.872 Million cell updates/sec

Title: US-09-854-731-4

Perfect score: 3260
Sequence: 1 MGOCYKGCASGRTRADGEGV.....LGFTKFLHGVTIRGSTRRH 623

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 segs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP:REMBL_17:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_prokaryote:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2862	87.8	625	10	P93520 zea mays (m
2	2831	86.8	607	10	Q41792 zea mays (m
3	2817	86.4	607	10	Q9FYU0 zea mays (m
4	2815.5	86.4	599	10	Q41791 zea mays (m
5	2251	69.0	452	10	Q23797 zea mays (m
6	2179	66.8	595	10	Q9ZU22 zea mays (m
7	1970	60.4	594	10	Q9SG12 zea mays (m
8	1948.5	59.8	594	10	Q9SG12 zea mays (m
9	1917	58.6	601	10	Q9FIM9 arabidopsis
10	1911	58.6	601	10	Q9SCS2 arabidopsis
11	1829	56.1	577	10	Q9LEU1 arabidopsis
12	1816.5	55.7	576	10	Q9LEU1 arabidopsis
13	1760.5	54.0	606	10	Q9FX86 arabidopsis
14	1749.5	53.7	415	10	Q9FX86 arabidopsis
15	1736.5	53.3	594	10	Q9XW6 arabidopsis
16	1736.5	53.3	599	10	Q9XW6 arabidopsis
17	1576	48.3	459	10	Q9XW6 arabidopsis
18	1153.5	35.4	571	10	Q48827 arabidopsis
19	1106.5	33.9	523	10	Q9SE25 oryza sativ

20	1080.5	33.1	512	10	Q9SE24 oryza sativ
21	1080	33.1	536	10	Q65644 arabidopsis
22	1072.5	32.9	523	10	Q9FKW4 arabidopsis
23	1039.5	31.9	564	10	Q9ZTU9 solanum tub
24	926	28.4	528	10	Q9FMP5 arabidopsis
25	923.5	28.3	583	10	Q9ZV15 arabidopsis
26	905.5	27.8	518	10	Q9AXA7 oryza sativ
27	903.5	27.7	529	10	Q42479 arabidopsis
28	895.5	27.5	548	10	Q9S7Z4 cucurbita
29	895.5	27.5	573	10	P93838 cucurbita p
30	889.5	27.3	540	10	Q81390 nicotiana t
31	887.5	27.2	548	10	Q9S786 marchantia
32	887	27.2	534	10	Q9ZPM0 mesembryant
33	886	27.2	531	10	Q41790 zea mays (m
34	886	27.2	554	10	Q49717 arabidopsis
35	883.5	27.1	639	10	Q9ZSA2 arabidopsis
36	874	26.8	980	10	Q9LORA zea mays (m
37	871.5	26.7	646	10	Q38870 arabidopsis
38	860	26.4	450	10	Q42396 arabidopsis
39	859.5	26.4	531	10	Q04123 zea mays (m
40	859.5	26.3	532	10	Q9ZSA2 arabidopsis
41	858.5	26.3	532	10	Q9XER6 solanum tub
42	853.5	26.2	465	10	Q41793 zea mays (m
43	852.5	26.2	560	10	Q9SCM0 arabidopsis
44	851	26.1	541	10	Q38868 arabidopsis
45	848.5	26.0	553	10	Q80700 arabidopsis

ALIGNMENTS

RESULT 1
ID P93520 PRELIMINARY; PRT; 625 AA.
AC P93520;
DT 01-MAY-1997 (TREMUR1. 03, Created)
DT 01-MAY-1997 (TREMUR1. 03, Last sequence update)
DE 01-JUN-2001 (TREMUR1. 17, Last annotation update)
DE CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE HOMOLOGY/CAM KINASE
DE HOMOLOGY/CAM KINASE
OS zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96236830; PubMed=8680305;
RA Lu Y.T., Hidaka H., Feldman L.J.;
RT *Characterization of a calcium/calmodulin-dependent protein kinase
RT homolog from maize roots showing light-regulated gravitropism.*;
RL Planta 199;18-24(1996).
CC 1-1 SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; S82324; ABA7181.1; -;
DR HSSP; P00518; IPHK.
DR Mendel; 13809; Zeama;1112;13809.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Euk.pkinase.
DR InterPro; IPR002290; Ser_thr_kin_actsite.
DR Pfam; PF00068; Pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 625 AA; 68789 MW; 00011D3F7484D0B8 CRC64;

Query Match 87.8%; Score 2862; DB 10; Length 625;
Best Local Similarity 87.7%; Pred. No. 2.5e-193;
Matches 561; Conservative 31; Indels 32; Gaps 7;
QY 1 MGOCYKGCASGRTRADGEGVTEHOSPPPPANGLPSTPPRQQAQAQVQTPRRR 55

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Db      1 MGOCYGRAGASSRADHDADPSGASVAPSPPLPANGAPLP-----ATPRRH 47
OY      56 GSKGSGTTPGHO-----TPG-VAMPSPYSGASPLPAGVSPSPARSTPRRFFKRPSPPS 110
Db      48 --KSGSTTPVHHQAAATPGAAAMPSPYPAGASPLPAGVSPSPARSTPRRFFKRPSPPS 105
OY      111 PAKIKATLAKRLGGGPKRGKTPEEGGVAGGCG-----GAADGAETERPLDKTEG 163
Db      106 PAKIKATLAKRLGGGPKRGKTPEEGGVAGGAGAGAGAGAAVGAADSAEADRPDLKTEG 165
OY      164 FSNFNGAKELGKVGKRGHGTCSAVVKGKGTVAVKITAKAKMTAISIEDVRE 223
Db      166 FANFNGAKYDLGKVGKRGHGTCSAVVKGKGTVAVKITAKAKMTAISIEDVRE 225
OY      224 VKILRALSGHNNLVKFFYDACEGLANYIWMELCEGELLDRLLARGRYTEEDAKAIYVQ 283
Db      226 VKILKALSGHNNLVKFFYDACEGLANYIWMELCEGELLDRLLARGRYTEEDAKAIYVQ 285
OY      284 ILSVAFCHLQGVHRDLKPENFLFTTRDENAPMKLIDFGLSDFTIRPDERLNDIVGSAVY 343
Db      286 ILSVAFCHLQGVHRDLKPENFLFTTRDESAPMKLIDFGLSDFTIRPDERLNDIVGSAVY 345
OY      344 VAPENVHRSYSMEADINSGVITTYILLGSRPPMARTESGIFRSVLRADPNFDDSPWPTV 403
Db      346 VAPENVHRSYSMEADINSGVITTYILLGSRPPMARTESGIFRSVLRADPNFDDSPWPTV 405
OY      404 SAEAKDFVRFLNKDYRKRMATVQALTPHMLDEOROLPLDILFRLIKOYLKATPLKRL 463
Db      406 SAEAKDFVRFLNKDYRKRMATVQALTPHMLDEOROLPLDILFRLIKOYLKATPLKRL 465
OY      464 ALKALSKALREBELLYLKLOFLKLEPRDGVSLDNFRTALTRYLDAMKESRYLEFLHAL 523
Db      466 ALKALSKALSEBELLYLKLOFLKLEPRDGVSLDNFRTALTRYLDAMKESRYLEFLHAL 525
OY      524 EPLAVRMDFEBCAAISPYLEALERWEELAGTAFQFEOEGNRYISVELAQEINLA 583
Db      526 EPLAVRMDFEBCAAISPYLEALERWEELAGTAFQFEOEGNRYISVELAQEINLA 585
OY      584 PTHYSIVODWIRKSDGKLNFLGFTKFLHGVITRGSNTRRH 623
Db      586 PTHYSIVODWIRKSDGKLNFLGFTKFLHGVITRGSNTRRH 625

RESULT 2
OY      041792 PRELIMINARY: PRT: 607 AA.
AC      041792;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      CDPK-RELATED PROTEIN KINASE.
OS      Zea mays (Maize).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC      Panicoideae; Andropogoneae; Zea.
OX      NCBI_TaxID=4577;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=IMBERD LINE H84; TISSUE=ROOT;
RX      MEDLINE=97072168; PubMed=8914977;
RA      Furumoto T., Ogawa N., Hata S., Izui K.;
RT      "Plant calcium-dependent protein kinase-related kinases (CRKS) do not
RT      require calcium for their activities.";
RL      FEBS Lett. 396:147-151(1996).
CC      -1. SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR      EMBL: D84508; BAA12692.1;
DR      HSP: P00518; 2PKK.
DR      Mendel: 13825; Zeam: 1112;13825.
DR      InterPro: IPR002048; EF-hand.
DR      InterPro: IPR000719; Euk.pkinase.
DR      InterPro: IPR002290; Ser_thr_kin_actsite.
DR      Pfam: PF00069; pkinase; 1.

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DR      SMART: SM00220; S_TKC; 1.
DR      PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR      PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW      ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ      SEQUENCE 607 AA; 67397 MW; E9B646E1C197CC3B CRC64;

Query Match
Best Local Similarity 86.8%; Score 2831; DB 10; Length 607;
Matches 553; Conservative 18; Mismatches 33; Indels 22; Gaps 7;

OY      1 MGOCYGRAGASSRADHDADVAP--PSPLPANGAP--TPGQRA-----TPGRR--K 47
Db      1 MGOCYGRAGASSRADHDADVAP--PSPLPANGAP--TPGQRA-----TPGRR--K 47
OY      59 GSGTTP-CHQTPGVAMPSPYPSGASPLPAGVSPSPARSTPRRFFKRPSPPAKHKA 117
Db      48 GSGATPVHHQAAATTPAMPSPYPAGASPLPAGVSPSPARSTPRRFFKRPSPPAKHKA 107
OY      118 TLAKRLGGGPKRGKTPEEGGVAGGAGGGAADGAETERLDTTPGSKNFKAKYELGKE 177
Db      108 TLAKRLGGGPKRGKTPEEGGAGV-----AUSAERERPLDTTFPANNFGAKYDLGKE 161
OY      178 VGRGHFGHTCSAVVKGKGTVAVKITAKAKMTAISIEDVRRREVKILRALSGHNNLV 237
Db      162 VGRGHFGHTCSAVVKGKGTVAVKITAKAKMTAISIEDVRRREVKILRALSGHNNLV 221
OY      238 KFYDACEDGLNVIYWMELCEGELLDRLLARGRYTEEDAKAIYVQILSVAFCHLQGV 297
Db      222 KFYDACEDGLNVIYWMELCEGELLDRLLARGRYTEEDAKAIYVQILSVAFCHLQGV 281
OY      298 HRDLKPENFLFTTRDENAPMKLIDFGLSDFTIRPDERLNDIVGSAVYVAPENVHRSYSMA 357
Db      282 HRDLKPENFLFTTRDESAPMKLIDFGLSDFTIRPDERLNDIVGSAVYVAPENVHRSYSMA 341
OY      358 DIVSIGVITYILLGSRPPMARTESGIFRSVLRADPNFDDSPWPSAEAKDFVRFLNK 417
Db      342 DIVSIGVITYILLGSRPPMARTESGIFRSVLRADPNFDDSPWPSAEAKDFVRFLNK 401
OY      418 DYKRMATVQALTPHMLDEOROLPLDILFRLIKOYLKATPLKRLALKALSKALREBEL 477
Db      402 DYKRMATVQALTPHMLDEOROLPLDILFRLIKOYLKATPLKRLALKALSKALREBEL 461
OY      478 LYKLOFLKLEPRDGVSLDNFRTALTRYLDAMKESRYLEFLHALPAYERMDFEBC 537
Db      462 LYKLOFLKLEPRDGLVSLDNFRTALTRYLDAMKESRYLEFLHALPAYERMDFEBC 521
OY      538 AAISPYLEALERWEELAGTAFQFEOEGNRYISVELAQEINLAPTHYSIVODWIRKS 597
Db      522 AAISPYLEALERWEELAGTAFQFEOEGNRYISVELAQEINLAPTHYSIVODWIRKS 581
OY      598 DCKLNFLGFTKFLHGVITRGSNTRRH 623
Db      582 DCKLNFLGFTKFLHGVITRGSNTRRH 607

RESULT 3
OY      09FYUO PRELIMINARY: PRT: 607 AA.
AC      09FYUO;
DT      01-MAR-2001 (TREMBLrel. 16, Created)
DT      01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      CALCIUM/CALMODULIN DEPENDENT PROTEIN KINASE MCK2.
OS      Zea mays (Maize).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC      Panicoideae; Andropogoneae; Zea.
OX      NCBI_TaxID=4577;
RN      [1]
RP      SEQUENCE FROM N.A.

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RA Lu Y.-T., Liang S., Wang L.;
RT "Cloning of a calcium/calmodulin-dependent protein kinase gene, MCK2
from maize."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF289237; MAG01179.1; -
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00069; pkinase.1.
DR SMART: SM00220; S_TKc.1.
DR SMART: SM00219; TYKc.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 607 AA; 67521 MW; 8907CD0F4DEC3810 CRC64;

Query Match 86.4%; Score 2817; DB 10; Length 607;
Best Local Similarity 87.9%; Pred. No. 3.6e-190;
Matches 550; Conservative 20; Mismatches 34; Indels 22; Gaps 7;

QY 1 MGQCYGR--GASGRADDEGVYEHOSPPRANGLPSTPPRQQAQAQAQVGTTRRRGSK 58
DB 1 MGQCYGRAGGASSRRADHDVAVP--PSPRPANGAP--TPPQQA-----TGRR--K 47
QY 59 SGSTTP-GHQTGVAMPSPYPSGASPLPAGVSPSPARSTRRFRFPFPSPAKHIKA 117
DB 48 SGSTTPVNHQAATTAMPSPYPAGASPLPAGVSPSPARSTRRFRFPFPSPAKHIKA 107
QY 118 TLAKRLGGKREKGTPEEGVGAGGGGGAADAEETPLDKTFGFSKNGAYELGKE 177
DB 108 TLAKRLGGKREKGTPEEGGAGV-----AADSAAERPLDKTFGFANNNGAKYDLGKE 161
QY 178 VGRGHEPHTCSAVVKKGEYKQGVAVVIAKAKMTAISIEDVREVKIILALSGHNLY 237
DB 162 VGRGHEPHTCSAVVKKGEYKQGVAVVIAKAKMTAISIEDVREVKIILALSGHNLY 221
QY 238 KFYDACEEDLVNLYIMELCEGSELLDRLLANGRYTEEDAKAIYVOILSVAFCHLGCV 297
DB 222 KFYDACEEDLVNLYIMELCEGSELLDRLLANGRYTEEDAKAIYVOILSVAFCHLGCV 281
QY 298 HRDLKPENFLFTTDENAEMKLDIFGLSDFTRPDERLNDIVGSAVYVAEVLHRSYSMEA 357
DB 282 HRDLKPENFLFTTDENAEMKLDIFGLSDFTRPDERLNDIVGSAVYVAEVLHRSYSMEA 341
QY 358 DIMSIGVITTYLLCGSRPFMAKTESGIFRSVLRADPNFDDSPWPTVSAEADFYKRFYLNK 417
DB 342 DIMSIGVITTYLLCGSRPFMAKTESGIFRSVLRADPNFDDSPWPTVSAEADFYKRFYLNK 401
QY 418 DYRKRMATVQALTRPMLRDEQROIPLDLIFRLIKOYLRAPIPLKRLAKLSKALREDEL 477
DB 402 DYRKRMATVQALTRPMLRDEQROIPLDLIFRLIKOYLRAPIPLKRLAKLSKALREDEL 461
QY 478 LYLKLOKFLLEPRGCVSLDNFRALTRYLTDAMKESVLEFLALAEPLAYRRMDEEFC 537
DB 462 LYLKLOKFLLEPRGCVSLDNFRALTRYLTDAMKESVLEFLALAEPLAYRRMDEEFC 521
QY 538 AAASIPVQLEALRMEETAGTAFOOFBOEGNRVTSVEELAOELNAPHYSTVODMIRKS 597
DB 522 AAASIPVQLEALRMEETAGTAFOOFBOEGNRVTSVEELAOELNAPHYSTVODMIRKS 581
QY 598 DGKLNFLGTFKFLHGVITRGSNTRRH 623
DB 582 DGKLNFLGTFKFLHGVITRGSNTRRH 607

RESULT 4
ID 041791 PRELIMINARY; PRT; 599 AA.
AC 041791;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CDPK-RELATED PROTEIN KINASE (FRAGMENT).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=INBRED LINE H84; TISSUE=ROOT;
RX MEDLINE=97072168; Pubmed=8914977;
RA Furumoto T., Ogawa N., Hata S., Izui K.;
RT "Plant calcium-dependent protein kinase-related kinases (CRKs) do not
require calcium for their activities."
RL FEBS Lett. 396:147-151(1996).
CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: D84507; BAI12691.1; -
DR HSSP: P00518; IPK.
DR Medel; 13824; Zeama; 1112; 13824.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00069; pkinase.1.
DR SMART: SM00220; S_TKc.1.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 599 AA; 66212 MW; ADF6193D37B51BFC CRC64;

Query Match 86.4%; Score 2815.5; DB 10; Length 599;
Best Local Similarity 89.4%; Pred. No. 4.3e-190;
Matches 547; Conservative 16; Mismatches 20; Indels 29; Gaps 5;

QY 26 SPPRANGLPSTPPRQQAQAQAQVGTTRRRGSKSGSTTPGHQ---TPG-VAMSPYPSG 80
DB 3 SPLPANGAPLP-----ATPRRH--KSSSTTPVNHQAATTGGAAMASPYRAG 47
QY 81 GASPLPAGVSPSPARSTRRFRFPFPSPAKHIKATLAKRLGGCKEETPEEGVG 140
DB 48 GASPLPAGVSPSPARSTRRFRFPFPSPAKHIKATLAKRLGGCKEETPEEGVG 107
QY 141 AGGGGG-----GAADGAETEPRLDKTFGFSKNGAYELGKEVGRGHGHTCSAVV 191
DB 108 AGAGAGAGAGAGAAVGAADSAEADRPDLDTGFAKNFGAKYDLGKEVGRGHGHTCSAVV 167
QY 192 KGEYKQGVAVVIAKAKMTAISIEDVREVKIILALSGHNLYKFYDACEEDLVNLY 251
DB 168 KGEYKQGVAVVIAKAKMTAISIEDVREVKIILALSGHNLYKFYDACEEDLVNLY 227
QY 252 VMEICEGSELLDRLLANGRYTEEDAKAIYVOILSVAFCHLGCVYHRDLKPENFLPTR 311
DB 228 VMEICEGSELLDRLLANGRYTEEDAKAIYVOILSVAFCHLGCVYHRDLKPENFLPTR 287
QY 312 DENAPMKLIDFGLSDFTRPDERLNDIVGSAVYVAEVLHRSYSMEADWISGVITTYLLC 371
DB 288 DENAPMKLIDFGLSDFTRPDERLNDIVGSAVYVAEVLHRSYSMEADWISGVITTYLLC 347
QY 372 GSRPFMAKTESGIFRSVLRADPNFDDSPWPTVSAEADFYKRFYLNKDYRKRMATVQALTH 431
DB 348 GSRPFMAKTESGIFRSVLRADPNFDDSPWPTVSAEADFYKRFYLNKDYRKRMATVQALTH 407
QY 432 PWLRDEQROIPLDLIFRLIKOYLRAPIPLKRLAKLSKALREDELTLKLOKFLLEPRD 491
DB 408 PWLRDEQROIPLDLIFRLIKOYLRAPIPLKRLAKLSKALREDELTLKLOKFLLEPRD 467
QY 492 GFVSLDNFRALTRYLTDAMKESVLEFLALAEPLAYRRMDEEFCAAISPYQLEALER 551
DB 468 GFVSLDNFRALTRYLTDAMKESVLEFLALAEPLAYRRMDEEFCAAISPYQLEALER 527

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QY 552 WEELAGTAFOOFEQGNRVISVEELAOELNLAPTHYSIVODWIRKSDGKLNFGTRKELH 611
D 528 WEELAGTAFOHFEQGNRVISVEELAOELNLAPTHYSIVODWIRKSDGKLNFGTRKELH 587
QY 612 GVTIRGSNTRRH 623
D 588 GVTIRGSNTRRH 599

RESULT 5
023797
ID 023797 PRELIMINARY; PRT; 452 AA.
AC 023797;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CALCIUM-DEPENDENT PROTEIN KINASE-RELATED KINASE (FRAGMENT).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=INBERD LINE H84; TISSUE=LEAF;
RX MEDLINE=97072168; PUBMED=8914977;
RA Furumoto T., Ogawa N., Hata S., Izui K.;
RT "Plant calcium-dependent protein kinase-related kinases (CRKS) do not
RT require calcium for their activities.";
RL FEBS Lett. 396:147-151(1996).
CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: D38452; BAA22410.1; -.
DR HSSP: P00518; 1PKH.
DR Mendel: 24438; Zeama:1112;24438.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR InterPro: IPR001245; Tyr_kin.
DR Pfam: PF00069; pkinase.1.
DR PRINTS: PR00109; TYRKINASE.
DR SMART: SM00220; S_TKc.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
FT NON_TER
SQ SEQUENCE 452 AA; 51789 MW; 42C3A5A76A3053P4 CRC64;

Query Match 69.0%; Score 2251; DB 10; Length 452;
Best Local Similarity 95.6%; Pred. No. 1.7e-150;
Matches 432; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

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QY 472 LREDELLYKLOFKLEPRDGVSLDNFRATLRTLDAMKESRYLEFLHALPLATYRM 531
D 301 LSEDELLYKLOFKLEPRDGVSLDNFRATLRTLDAMKESRYLEFLHALPLATYRM 360
QY 532 DFEFCAAAIISPYOLEALERMEELAGTAFOOFEQGNRVISVEELAOELNLAPTHYSIVO 591
D 361 DFEFCAAAIISPYOLEALERMEELAGTAFOHFEQGNRVISVEELAOELNLAPTHYSIVO 420
QY 592 DWIRKSDGKLNFGTRKELHGVITRGSNTRRH 623
D 421 DWIRKSDGKLNFGTRKELHGVITRGSNTRRH 452

RESULT 6
09ZU22
ID 09ZU22 PRELIMINARY; PRT; 595 AA.
AC 09ZU22;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE HYPOTHETICAL 66.6 KDA PROTEIN.
GN T3A4.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Rongning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC T3A4 genomic sequence."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: TO EF-HAND FAMILY.
DR EMBL: AC005819; AAC69927.1; -.
DR HSSP: P24941; 1CKP.
DR Mendel: 34144; Arabid.1112;34144.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_kin_actsite.
DR Pfam: PF00036; efhand.1.
DR Pfam: PF00069; pkinase.1.
DR SMART: SM00220; S_TKc.1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
KW ATP-binding; Calcium-binding; Hypothetical protein;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 595 AA; 66599 MW; C6D9C158BBA41A39C CRC64;

Query Match 66.8%; Score 2179; DB 10; Length 595;
Best Local Similarity 68.3%; Pred. No. 3e-145;
Matches 426; Conservative 71; Mismatches 93; Indels 34; Gaps 7;

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OY		239	FYDACEDELANTAYIMEWCEGEGELLDRIIANGRGYTEEDAKAIYOQLISVAFCILQGVH	238
OY	:		: :	
Dd		210	YYDACEDANNVITYMEWCDSGELLDRILIARGGKIPEDDAKAIVOLLTVASFCHLQGYH	265
OY		299	RDLAPENFLFTTRDENAMPMKLIDFGLSDFIIRPDERLNDDIVGSAYVAPEVLHRSYSMEAD	358
Dd		270	RDLRPENFLFTSSRDSDDLTKLIDEGLSPDIRPRDELRNDIYGASAVYAPEVLHRSYSLEAD	329
OY		359	IWSIGVTITYLCCSRRPMATTESGIFPSVLRAPPNDDSDWPVVSALDPFYKRFINKD	418
Dd		330	IWSIGVTITYLCCSRPMATTESGIFPTVLTREPNVDVPDWPCSSSEGDVFYRLINKD	389
OY		419	YRKRTTAAVQALTTHMPLRDPOQRQIIDLIIFPLIKOYLRATPKLKALKALKALKEDELL	478
Dd		390	YRKMSANQAITHMLRDRSDSVIFLDIIITLVKAYIAIHAPLRRAALKALKALKTENEVL	449
OY		479	YLKIQFKLEER-RDGFSVSLDNFRATRYTLTDAMESRVLEEHLALEPLAYRRMDFEFFC	537
Dd		450	YLRAQFMILGNKKDGSVSLENFKTALMQNATDARESVEPIELHTMESLYARKMYFEFFC	509
OY		538	AAASPYOLAELEMEREEETAGTAFOOEBOEGRVTSVEELOELMALPHHSIVODWTIRS	597
Dd		510	AAAISIHOLEAVDAWEELATATGFOHFEPETRNRVITTBELARELVGASANGLHDWRSS	565
OY		598	DGKIINFGEFTKFELHGVTIRGSNTA 621 : : :	
Dd		570	DGKLSYLGTFKFLHGVTILRAAHAR 593	
RESULT		7		
OYSG12	PREDIMINARY;	PRT;	594 AA.	
AC	OYSG12;			
DT	01-MAY-2000 (TREMBLrel_13, Created)			
DT	01-MAY-2000 (TREMBLrel_13, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel_17, last annotation update)			
DE	POTATIVE CALCIUM DEPENDENT PROTEIN KINASE. TG12.7 OR FZK15.230.			
OS	Aralidopsis thaliana (Mouse-ear cress).			
OC	Eurariota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;			
OC	eucosids II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCGI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-CV, COLUMBIA;			
RA	Ltn X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D., Maliti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barstead M.E., Bowman C.L., White O., Nieman W.C., Fraser C.M.; Arabidopsis thaliana chromosome I BAG TG12 genomic sequence.";			
RL	Submitted (Jan-2001) to the EMBL/GenBank/DDBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Rieger M., Gebel C., Mueller-Auer S., Schaefer M., Zipp M., Meves H.W., Lemke K., Mayer K.F.X., Queffier F., Salanoubat M.;			
CC	-1- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.			
DR	EMBL; AC012329; AAG5216.1; -			
DR	EMBL; AL132956; CAB66416.1; -			
DR	HSSP; Q63450.1A06.			
DR	InterPro; IPRO000719; Euk_Pkinase.			
DR	InterPro; IPRO02290; Ser_thr_kin_actsite.			
DR	SMART; SM00220; S_TKC; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
KW	PROSITE: P500108; PROTEIN_KINASE_ST; 1.			
KW	ATP-binding, kinase, serine/threonine-protein kinase, transferase.			
SQ	SEQUENCE 594 AA; 66371 MW; 28170246FB708F89 CRC64;			

Query Match	60.4%;	Score 1970;	DB 10;	Length 594;
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Best Local Similarity 62.8%; Pred. No. 1.6e-130;
Matches 391; Conservative 81; Mismatches 117; Indels 34; Gaps 8;

QY	1	MGOCYGGASGRTADDDGGVTEHOSPPRPPANGTPEPRBOAOAOAOVOTPPRRGSGSG	60
Db	1	MGHCYSNRISIVYDDDE-----IPSS-----ATAQOLRBNHONHNNHSSS	39
QY	61	STTPGHOTPGVAMPSPYR-SCGASPLDAGVSPSPARSTPRRFKKRPPRPPSAKHIKATL	119
Db	40	SSIP--OSPAPSEVNPANISFPFOSPLDAGVAPSPAR-TPRKRFKWPERRPPSPAKPIAAL	96
QY	120	AKRIG-GGKPEEGTIPREGGVAGCGGGGGAADGAETRPDLTKPFGEKNKGAYETLGEV	178
Db	97	RRRKGTAPHPDGPPIEDSEAGSGGGG-----ER-LDKNGEFAKNDEGKTGLREV	148
QY	179	GRGHGHTCSAVVKKGEYKQGVAVKIIIAKAKMTAISIEDVREXVITLALSGHNLYK	238
Db	149	GRGHGHTCMYAKAKKGIKQGTAVKIIISKMTSALISEDVREXVITLALSGHMYK	208
QY	239	FYDACEGLNVIYMEICEGSELLDRLLARGRTYEDDAKIYVQIIISVAFCHLGSVH	238
Db	209	FYDFEEDSDNFVYMEICEGELLDSILARGRPFEAKRILOVIIISAFPHLGSVH	268
QY	299	RDLPENFLFTTRDENAPMKLIDFGLSDFTIPDRRLNDIYSAVYAPEVLHNSYMEAD	358
Db	269	RDLKPENFLFTSKNEDAVLAKIIDFGLSDYARFDORLNDVGSATVYAPVULHNSYSTAD	328
QY	359	IMSIGVITYIILCGSRPFMAWTSGETRSYLRADPNFDDSPWTVSAEAKDFYKRLNKD	418
Db	329	IMSIGVITYIILCGSRPFYGTESAIERCVLRADPNFDDLPWPSIPIAKDFYKRLNKD	388
QY	419	YRKWMTANQALTHRWLNDQEQIPLDILIRLIQYIARTRPKLYAKALASKALREBEL	478
Db	389	HRKRRTAAQALAHWLNDENPGLLLDSEYKLVKYSIRASFPAAKLSKALIREELY	448
QY	479	YLKIQFLKLEBRDFVSJLNDERTALTRITLPAKESVLEFLIALLEPLATVARNDFEECA	538
Db	449	FLKQFMLEBRDEDSGLHNLNTTALTRITADYMAIESLRLPINMMQPLAKKIDFEECA	508
QY	539	LAISPYQLEALERMEIAGTAFQOEEOBGNRVISVEELAEQLEALAPHYSTIVODMTRKD	598
Db	509	ASVSYQLEALEEMEOLATVAFEHFESESGRAISVOELAEEMSGIPNAPYPLDKMIRSLD	568
QY	599	GLNPLDGTGKFLGHVGTGSTR 621	
Db	569	GLNPLDGTAKFLGHVTVKSSSR 591	

RESULT	8		
QOFIM9			
ID	QOFIM9	PRELIMINARY;	PRT; 594 AA.
AC	QOFIM9;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	CALCIUM DEPENDENT PROTEIN KINASE-LIKE PROTEIN.		
OS	Arabidopsis thaliana (Mouse-ear cress).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;		
OC	eumastids II; Brassicales; Brassicaceae; Arabidopsids.		
OX	NCBI_TaxID=3702;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=COLUMBIA;		
RX	MEDLINE=99156233; PubMed=10048486;		
RA	Asamitsu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,		
RA	Tabata S.;		
RT	Structural analysis of Arabidopsis thaliana chromosome 5. VIII.		
RT	Sequence features of the regions of 1,081,958 bp covered by seventeen		
RT	physically assigned P1 and TAC clones."		
RL	DNA Res. 5:379-391(1998).		
DR	EMBL; AB016884; BAB11236.1; -		
DR	EMBL; AB025641; BAB11236.1; JOINED.		

Query Match 55.7%; Score 1816.5; DB 10; Length 576;
Best Local Similarity 57.3%; Pred. No. 9, 6e-120;
Matches 356; Conservative 95; Mismatches 109; Indels 63; Gaps 9.

QY 1 MGQCYGKAGSGRTADDEGVYTEHQSPPNPANGPSPTRPROAOAOAOYGTTPRRSGSG 60
Db 1 MGICHGK-----PVEQGS-----KSLPVSGEINENAPNTNQ----- 30
QY 61 STTPGHOTPCVAMPSPYPPSGGASPLDAGVSPSA-----RSPRRFFKPPPPSPAKHI 115
Db 31 ---PPASSGCFPPYSP-----SPVSLKRSQSPSSVSSVSTPLRITFKRPPFPSPAKHI 81
QY 116 KATLAKRLGGKKEGTITEEGGVGAGGGGGAADAETERPDLDTFGFGSKNFGAYELG 175
Db 82 RAFLARRYSVKNNEVSIPE-----GKEEIGLDSFGSGSKFPASHYED 126
QY 176 KEVGRGHFGTCGAVYKKGEGYKQTVAAVKAIAKAKTTAISTEDYAREVKILRALSGHNN 235
Db 127 GEVGRGHFGTCGAKKQKSLGQAEVAVVIFPKSKMTTAIAIEDVSREVKMLRALTLGHKN 186
QY 236 LVNFYDACEGLGVVYIMELCEGEGELDLRLTARGRYTEEDKATVVOILSVYACHTLGG 295
Db 187 LVGFYDAFEDDEVVYIMELCKGGELDLKTLIIRGGKYSDDOKKVVQILSVYACHLGG 246
QY 296 VYARDLKPENFLFTTRDENAPMKLIDFGLSDFTRPDERLNDIVGSAYYVAEVLHRSYSM 355
Db 247 VYARDLKPENFLFTSTDEKSPPLKALIDFGLSDVYKPDERLNDIVGSAYYVAEVLHRTYGT 306
QY 356 EADWISIGVITYILLGSGSPFWARTESGFERSVLADNPFDOSPPMYTSAEKDPVYKFL 415
Db 307 EADWISIGVIAVILLGSGSPFWARTESGFERSVLADNPFDOSPPMYTSAEKDPVYKFL 366
QY 416 NNDYRRKRAVQAALTHPWL-RDEGQIPLDILIFFLIKQYLRAPLKLALKAALSKALRE 474
Db 367 NNDYRRKRLAQAALCHPWLGVSHKLTISDMITVYLVVYIMSTLSRKSALALAKTLTY 426
QY 475 DELLYLKLQFLKLEP-RDGFVSLDNFRPLAPYLTDARKKESVLEFLALPLAYRRDF 533
Db 427 PQLATIREGFTLLGGSKNGIYIMQYKATILKSSTDANKKDSVDFVPMHISCLQTKLDE 486
QY 534 EEFCAALISPVQLEALERNMETAGTAFOOFDEGNRIVSVEELAOELNLAFT--HYSTYQ 591
Db 487 EEFCAALISPVQLEALERNMETAGTAFOOFDEGNRIVSVEELAOELNLAFT--HYSTYQ 546
QY 592 DWIRKSDKLNLFPTKFLHGVTIR 616
Db 547 DWIRKSDKLNLFPTKFLHGVTIR 571

RESULT 13
Q9FX86 PRELIMINARY; PRT; 606 AA.
AC Q9FX86
ID Q9FX86
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE PUTATIVE CDPK-RELATED PROTEIN KINASE.
GN F14J22.18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_Taxid=3702;
LN [1]
RM
RP SEQUENCE FROM N.A.A.
RA Federicipliel N.A.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA Alfari H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA Gonzalez A., Kremetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA Luros S., Schwartz J., Shinn P., Toriumi M., Theotokis A., Vaisotskaia V.S.,
RA Walker M., Yu G., Ecker J., Thinn P., Toriumi M., Theotokis A., Vaisotskaia V.S.,
RL Submitted (SEP-2000) to the EMBL/Genbank/DBJ databases.
EMBL: AC011807; AAG13044.1; -

DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR002719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR InterPro: IPR001245; Tyr_kin.
 DR Pfam: PF00069; pkinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TyKc; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR ATP-binding; Kinase; Transferase.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 606 AA; 67972 MW; 535329AD5F89B14C CRC64;

Query Match 54.0%; Score 1760.5; DB 10; Length 606;
 Best Local Similarity 59.7%; Pred. No. 9.1e-116;
 Matches 357; Conservative 74; Mismatches 104; Indels 63; Gaps 11;

QY 64 PGHGTGVAMPSPYPSGG-ASPLPAGVSPRAR-----STPRFFK 103
 DB 32 PDKS-PIPTPSAKASPPFPYTPSPARRRNSKSDVGGGSKSLTSTPLQLR 88
 QY 104 RPPPPSPAKHAKATLAKRLGCGKPKETI-----PECGVAGGGGGGAD 150
 DB 89 RAHPSPAKHAKAALRRRG---KKEALSGVTQLTTEVPQREBEVQ----- 135
 QY 151 GAETPRPLDTGFGSKNFGAKYELGKEVGRGHTCSAAVVKKEGKQGVAAKIIAKAK 210
 DB 136 -----LKRFGFGSKFHFHSGELGEGHGYTCSAKFKGELKGQVAAKIIIPKSK 188
 QY 211 MTTAISIEDVRRREVKKILRALSGHNNLVKFPDAGEDGLNVYIMELCGEGLLDRILARGG 270
 DB 189 MTTAISIEDVRRREVKKILRALSGHNNLVKFPDAGEDGLNVYIMELCGEGLLDRILARGG 248
 QY 271 RYTEDAKAIYVQILSVAFCHGQVVRDLKPENFLTTEDENAPMKLIDFGISDFIRP 330
 DB 249 KYSEDAKAIYIQLINNVACHGQVVRDLKPENFLTTEDENAPMKLIDFGISDFIRP 308
 QY 331 DEFLNDIVGSAYVAPEVLRHRSYMEADWSIGVITYILLGSRPFMAFTESGIFRSVLA 390
 DB 309 DEFLNDIVGSAYVAPEVLRHRSYMEADWSIGVITYILLGSRPFMAFTESGIFRSVLA 368
 QY 391 ADNFDDSPMTVSAEAKDFKRLNDRKMTAVOALTHPMLR--DEGROIPLDLIF 448
 DB 369 ADNFDDSPMTVSAEAKDFKRLNDRKMTAVOALTHPMLR--DEGROIPLDLIF 428
 QY 449 RLKQYLRATPLKRLAKLSKALREDELLYLKQFLLEP-RDGEVSLDNFTALRYL 507
 DB 429 ROKKAYLRSSSLKRALRALSKLTLIDELLYLKTQFSLAPNKGDLTMTIRALASNA 488
 QY 508 TDMAKSRVLEFLHLEPLAYRRMDPEEFCAAIISPYOLEALERMEIAGTAQOEBOEG 567
 DB 489 TEAKMSRVRLEFLHLEPLAYRRMDPEEFCAAIISPYOLEALERMEIAGTAQOEBOEG 548
 QY 568 NRVISVEELAQELINLAPT--HYSIVODMIRKSDGKLNFLGFTFKLHGVTIR--GSNRR 621
 DB 549 NRVISVEELAQELINLAPT--HYSIVODMIRKSDGKLNFLGFTFKLHGVTIR--GSNRR 606

RESULT 14
 ID 081088 PRELIMINARY; PRT; 415 AA.
 AC 081088;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE CDPK-RELATED PROTEIN KINASE (FRAGMENT).
 GN CRK1
 OS Tradescantia virginiana (Virginia spiderwort).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Commelinales; Commelinaceae;
 OC Tradescantia.
 OX NCBI_TaxID=59016;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE-STAMEN HAIR;
 RA Sukanya R., Molniak S.M.;
 RT "A CRK like sequence from Tradescantia virginiana."
 RC Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RL -1 SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC -1 SIMILARITY: TO EF-HAND FAMILY.
 DR EMBL; AF009337; AAC24961.1; -.
 DR HSSP; P00523; 2PTR.
 DR Mendel; 31742; Travl; 1112; 31742.
 DR InterPro: IPR002048; EF-hand.
 DR InterPro: IPR002719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR InterPro: IPR001245; Tyr_kin.
 DR Pfam: PF00036; efhand; 2.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS500108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Calcium-binding; Serine/threonine-protein kinase;
 KW Transferase.
 FT NON_TER 1 1
 SQ SEQUENCE 415 AA; 47875 MW; 623EF3DE54EDB21 CRC64;

Query Match 53.7%; Score 1749.5; DB 10; Length 415;
 Best Local Similarity 81.5%; Pred. No. 3.1e-115;
 Matches 339; Conservative 37; Mismatches 35; Indels 5; Gaps 3;

QY 212 TTTAISIEDVRRREVKKILRALSGHNNLVKFPDAGEDGLNVYIMELCGEGLLDRILARGG 271
 DB 1 TTTAISIEDVRRREVKKILRALSGHNNLVKFPDAGEDGLNVYIMELCGEGLLDRILARGG 60
 QY 272 YTEDAKAIYVQILSVAFCHGQVVRDLKPENFLTTEDENAPMKLIDFGISDFIRP 331
 DB 61 YTEDAKAIYVQILSVAFCHGQVVRDLKPENFLTTEDENAPMKLIDFGISDFIRP 120
 QY 332 ERLNDIVGSAYVAPEVLRHRSYMEADWSIGVITYILLGSRPFMAFTESGIFRSVLA 391
 DB 121 ERLNDIVGSAYVAPEVLRHRSYMEADWSIGVITYILLGSRPFMAFTESGIFRSVLA 180
 QY 392 DPNFDDSPMTVSAEAKDFKRLNDRKMTAVOALTHPMLR--DEGROIPLDLIF 451
 DB 181 DPNFDDSPMTVSAEAKDFKRLNDRKMTAVOALTHPMLR--DEGROIPLDLIF 240
 QY 452 KOYLRATPLKRLAKLSKALREDELLYLKQFLLEP-RDGEVSLDNFTALRYL 510
 DB 241 KLYLRATPLKRLAKLSKALREDELLYLKQFLLEP-RDGEVSLDNFTALRYL 300
 QY 511 MKSRVLEFLHLEPLAYRRMDPEEFCAAIISPYOLEALERMEIAGTAQOEBOEG 570
 DB 301 MKSRVLEFLHLEPLAYRRMDPEEFCAAIISPYOLEALERMEIAGTAQOEBOEG 360
 QY 571 ISVEELAQELINLAPT--HYSIVODMIRKSDGKLNFLGFTFKLHGVTIR--GSNRR 623
 DB 361 ISVEELAQELINLAPT--HYSIVODMIRKSDGKLNFLGFTFKLHGVTIR--GSNRR 415

RESULT 15
 ID 09XG6 PRELIMINARY; PRT; 594 AA.
 AC 09XG6;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE CDPK-RELATED KINASE 2 (FRAGMENT).
 GN CRK2
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-CV, COLUMBIA; TISSUE-SEEDLING HYPOCOTYL;
 RA Choi J.H., Lala H.;
 RT "CDPK-related kinases in Arabidopsis";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF153352; AAD38059.1; -.
 DR HSSP: O63450; 1A06.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_kin_actsite.
 DR InterPro: IPR001245; Tyr_kin.
 DR Pfam: PF00069; pkinase_1.
 DR PRINTS: PR00109; TYRKINASE.
 DR SMART: SM00220; S_TKC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferrase.
 FT NON_TER 1
 SEQUENCE 594 AA; 66757 MW; C21D97BCAD2440B CRC64;

Query Match 53.3%; Score 1736.5; DR 10; Length 594;
 Best Local Similarity 59.9%; Pred. No. 4.3e-114;
 Matches 355; Conservative 75; Mismatches 120; Indels 43; Gaps 9;

QY 52 PRRGSGSGSTTPGHQTPGVAMPSPYPSGASPLPAGVSPSPAR----- 95
 DB 14 PKDAVLQNDSDTPAH--PGKSPVRSPPAVKSPFPFPYTPSPARHRRKNSRDGGGSEKS 71
 QY 96 --STPRRFRKRPSPSPAKIKATLAKRLGGKPKRGKTIPREGGVAGAGGGGADGAE 153
 DB 72 VTSTPLQLAFAHPSPSPARHIDVLR--KEKKAALP-----AARQKEE 117
 QY 154 TERP--LDKTFGSKNFGAKYELGKEVGGRGHFGHTCSAVVKKGEYKQTVAVKIKAK 210
 DB 118 EEREVEYGLDKRFGSKELSGRIELGEGIRGHGYTCSAKFKGELKDQEVAVKVIPIKS 177
 QY 211 MTTAISTEDVAREYKILRALSGHNNLVKFTDACEGDLNVIYIMELCEGELLDRILARG 270
 DB 178 MTSAISIEDVAREYKILRALSGHNNLVKFTDACEGDLNVIYIMELCEGELLDRILARG 237
 QY 271 RYTEEDAKAIYVOILSYVAFCHLOGVVRDLKRPENLFTTRDENAPMKLIDFGISDFIRP 330
 DB 238 KYSDDDAKAVLIQILNVAFCCHLDGVVVRDLKRPENLFTSKENSMKLVIDFGISDFVRP 297
 QY 331 DERLNDIVGSAYVYAPVFLHRSYSMEADIVSIGVITYILLGSRPEWARTESGIFRSVL 390
 DB 298 DERLNDIVGSAYVYAPVFLHRSYSMEADIVSIGVITYILLGSRPEWARTESGIFRSVL 357
 QY 391 ADPRFDSRPPTVSAEKADVVKRFLNKDYRKMTAVOALTHPWLRDEQR-QIPDLILIFR 449
 DB 358 ADPSFDEPPPPSLSEFAKDKVLRFLYKDPKRMTASQALMHPWLAGYKKIDIPDILIFK 417
 QY 450 LIQVLAATPLKRLALKALSKALREDELTYLKIOLFLLRP-RDGFVSLDNFRALTIRYL 508
 DB 418 QIKAYLRSSSLRKRAALMALSKLTITDELTYLKIOLFLLRP-RDGFVSLDNFRALTIRYL 477
 QY 509 DAMKESRVLEFLHALPFLARRMDFEEFCAAATSPQLEALERMEETIAGTAFOQFEQGN 568
 DB 478 EAMKESRIPDFLLALNGLDQYKMDFEFCASISVGHESLDCWEOSIRHAYELFEMNGN 537
 QY 569 RVISVEELAOELNLA--PTHTSIVODWIRKSDGKLNFLGFTKFLHGVTIRGS 618
 DB 538 RVIVIEELASELGVSSIPVH-TILNDWIRHTDGKLSFLGFTVXLLHGVSSTROS 589

Search completed: May 2, 2002, 08:47:59
 Job time: 628 sec

Db	1611	AACTTTGTATCTTAGTGTGAGTTTAAAGCGCTTGAACCCAGAGATGGCTTCGTGCAC	1670
Qy	1681	ttgacaacttccgcgcgcgcactaaacgcgatatttcaactgcatgcatgaagaatccgaagg	1740
Db	1671	TGCAAACTTTTCGGACGGCTGTGACAAAGATCTCACTCAAGTCAGCCATGAGAAATCAAGG	1730
Qy	1741	ttcttgaatttttgcgtgctgtgaaccacttgcataaagaagaatgaccttttgaagat	1800
Db	1731	TTCTWGAATTTTCAGATCCGTTGGAAACCTTGGCTTACAGAAAGATGACCTTTGAGAT	1790
Qy	1801	tcgtgcgcgcgaactcaactgctcttaacagcttgaagaccctgaaaggtgggaagagatgt	1860
Db	1791	TCTGTGCTGCAGCAATCAACCCGTTACCACTGGAAGCTTTTGGAAAGTGGGAAGAAATG	1850
Qy	1861	ctggaacagcttcccaagaatttgaacaagaagggaaccagatcatatcaatgtagaagat	1920
Db	1851	CTGGAACAGCTTTTCAGCAGCTTTGAAACAAGAGGGCAACGAGTTATATCAATTTAGAGAGT	1910
Qy	1921	ttagcaagaagaattaaacttctgctcccaacttaactcatcgttcaagaactgtagaagaa	1980
Db	1911	TAGCACAGAACTAAATCTCCGCGCACACATTACTCCATTTGTGCAGAACCTGATCAAGAA	1970
Qy	1981	aatccagagggaagctaactttctcggttttacaaaattttacatgctgcacaaataa	2040
Db	1971	AATCGAGCGGCAAGCTTAACTTCTTGGCTTACCAAAATTTTGGACGGTGTCAAGATAC	2030
Qy	2041	ggggctcaatacaagaacgagataaagatattgcaagaagaatgatatcttctctt	2100
Db	2031	GGGGTTCAAAATACAAAGACAGACATAACAGATGCAAACTGTA-----TTGCGTT	2079
Qy	2101	ctaattttaaagc--cgctcaatatgtagccctgattgattgttccctccctgctctc	2157
Db	2080	CTAATTTGAAGCGCTCTCAATCATATATATGAGCCCTGATTTGCTGTTACCTCGCCCTGCCC	2139
Qy	2158	atccctctggttcaatgatcatcatattcttctgtgtgctgctgctgctgtgtgtcatcat	2217
Db	2140	TGCCCCGTAAGTGTGTCATGACCAATCCCTTTGGTGTGATGC-CCCTCCCGGTGTGGCCGT	2198
Qy	2218	agttcttgcagagatacatgataagaatctcttctgtaagaatcgaatgcatgttgtt	2277
Db	2199	CGTACTTTTGTGAGAGTATCATATGATAAAGATC-CTTGTAATGGCGAAATCATATGCTTTCCT	2257
Qy	2278	caagaataatagtgcatcgtgtgtcttttt 2308	
Db	2258	CAAGAAATATATAGTGCATTTGTTCTTTT 2288	
RESULT	2		
MZECDEKA			
LOCUS	2140 bp	mRNA	PLN 06-FEB-1999
DEFINITION	Zea mays mRNA for CDPK-related protein kinase, partial cds, clone zmcRKL.		
ACCESSION	DB4507.1	GI:1313906	
VERSION	DB4507		
KEYWORDS	CDPK-related protein kinase; calcium-dependent protein kinase-related kinase; CRK.		
SOURCE	Zea mays (strain:inbred line H84) root cDNA to mRNA, clone_1ib:lambda gtl0 clone:zmcRKL.		
ORGANISM	Zea mays		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.		
AUTHORS	Furumoto, T., Ogawa, N., Hata, S. and Izui, K.		
TITLE	Direct Submission		
JOURNAL	Submitted (27-APR-1996) to the DDBJ/EMBL/Genbank databases.		
REFERENCE	Tsuayoshi Furumoto, Kyoto University, Graduate School of Agriculture Lab. of Plant Physiology, Sakyo-ku, Kyoto, Kyoto 606-01, Japan (E-mail:tsuyokais.kyoto-u.ac.jp, Tel:075-753-6142, Fax:075-753-6146)		
AUTHORS	2 (sites)		
TITLE	Furumoto, T., Ogawa, N., Hata, S. and Izui, K.		
REFERENCE	Plant calcium-dependent protein kinase-related kinases (CRKs) do		

not require calcium for their activities
 FEBS Lett. 396 (2-3), 147-151 (1996)

JOURNAL MEDLINE 9/7072168

FEATURES

source location/Qualifiers

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/organism="Zea mays"

/strain="inbred line H64"

/db_xref="taxon:4577"

/clone="ZmCRK1"

/clone_id="Lambda gt10"

/tissue_type="root"

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/note="Does not require calcium for its activity (by similarity)"

/codon_start=1

/product="CDPK-related protein kinase"

/protein_id="BA12691.1"

/db_xref="GI:1313907"

/translation="PPSPDIPANCAPIPLATPRNHSKSGSTPYVHNHOATPGAAAMPSPYPAGASDLPAPAVSPSPARSTPRFRFKFRPPSPAKIKATLAKRLRGKKEETTPPEEGGAGAGAGAGAGAGAAGAAUASAEADRLDTFGANFNGAKYDGEKVGKHFGHTGSAVYKGGAGKHGTVAVKIISKAKMTTASISDVREYVILKALSGHMLVFEPDACEDLANVYIVMELECEGELDIRILARGRYTEDAKAIYVILSVAFCHLGVNHRDLKPNPLFTTDESAAPMKLIDFGSLDRFPERLNDYGSAYVAPEVLHRSYEMEDLINSGLVTYLLICSGRPMAPTESGIRSVYRAPNDPSPSPVSAKQPVKPRFLNKDYRRKRAVDALTHPMLRDRORIPDLILFRILVKOTLRPTPKRLAKRLSKALSDLLYLRLQFVLELRDRGVSLDNFRALTRYSTDAMKESVLEFHLEPLARKKMIFEECCAAASPYOLEALEMEIEIAGTAFQHPEDGGRNIVSELEAOELINTLAPTHYSIVYQDWIRKSGKINFGFTKFLHGVIRGSTRRH"

BASE COUNT 506 a 544 c 572 g 518 t

ORIGIN

Query Match 55.4%; Score 1314.2; DB 8; Length 2140;
 Best Local Similarity 81.9%; Pred. No. 1.2e-188;
 Matches 1593; Conservative 0; Mismatches 308; Indels 44; Gaps 5;

408 ggcgtggccgagcgcttaccgctccgggggcgcgagcccgctgcgcgccgggtgtgcgcg 467
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 115 GCGTGGCTAGCGCCCTACCGCGGCGCGGCGGCGACCCGCGCTCCGCGGCGGCGTGCgcg 174
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 468 tgcgcgcgaggtgcagcgcccgagaggttcttcaagcgcgcttccgcgcgcgtgcgcg 527
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 175 TCGCGGCGCGGCTCCACGCGCCCGGAGGTTCTTCAAGCGGCGCCTTCCGCGCGCTCGGCC 234
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 528 gccaaacacataaaggcgcagcgtcgcccaagagcgtgtgtggggggaagcccaagaaagg 587
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 235 GCCAAGCACATCAAGGCCACGCTCCCAAGCCCTCGCGGGGGGCGCAAGCCAGAGGCG 294
 |||||
 588 acgataccggaagagggagcgctgggcgttg-----c 620
 |||||
 235 ACCATAACCGGAGAGGCGCGCGGCGGCGCGGCGCGGCGCGGCGCGCGCGCGCGCGCC 354
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 621 ggcgcgcgtgtgagggcgcgatggggcgcgagacgagagagcgcattggacaaagcgttc 680
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 355 GCGCGGCGCGTGTGGTGGCGCGGATTCGCGCGAGGCGGACCGCGCGCTGGACAACGTTTC 414
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 681 gggtctcgagaacttcggcgcgaagtacgaagctcgggaaggaaggttgggaggggacac 740
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 415 GCGTTTCGCCAAGACATTGGGGCGCAAGTACGATCTCGGGAAGAGAGTCCGGAGGGGCCAC 474
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 741 ttccgacacacttgcctcgcgctgcgtcaagaaggcgagtaacaaggacagacgctgcgc 800
 |||||
 475 TTTGGCCACACTGCTCGCGCGCTGCTCAAGAGAGGCGGACACAAAGGCCATACCGTCCGC 534
 |||||
 801 gtcaagatcatcgcaaaagctaaagtacgaacgagcaataatccattgaagatgttcgtaga 860
 |||||
 535 GTCAGATCATCTCCAAAGCTAAGATGACAAAGCGCATTTCCATTGAAGATTTCTGTAG 594
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 861 gaagtaaaattttagagcgctatcagaaggacaaataatcgttcaaatctatgataga 920
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 595 GAGGTCAGAAATTTTGAACCCCTATCAGGGCGACGATAAATCTGTCAGATTCTATGATGGA 654

OY	921	tgtagagatggccctcaatgtctacatctgtcatgtgaattatgtgagggagagaattccta	980
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OY	1101	ccagagagaattctcttcttccaaaccgggagtgaataatgcccctcaatgaattgtattctt	1160m
Db	835	ccagagaatttttcttcttccaaacaaaggaagaaagggcctccatnagaattgtattctt	894
OY	1181	ggtcctctgtattcatcttagaccagatggaaggtcctaattgatctgttggaagtcatat	1220m
Db	895	ggtctgtcagattttttatttaaccnagatgaanagcctaaatgatattgttggaaagtcttat	954
OY	1221	tatgtcccccagaggtcttaccagaatacatatagatgtgaagcagacattcgtgaagta	1280m
Db	955	tatgttgctccagaggtttatcacagatcatatagatgatgaagcagacatttggagttata	1014d
OY	1281	ggtgtcataacgtcatctctgcctctgtgcagtcggcaattcttgggacgaacagaatca	1340m
Db	1015	gggtttatnataatnacttctgtctgtgagagtcggccacttcttggggacaaagacatact	1074d
OY	1341	ggaataatccgaatctgtgttcttgagagcgtgatacccaactttgatcttaacccgtggctca	1400m
Db	1075	gggatcttccgggtccgatttgtagggcctgatcccaatttttgacagattccacatggccttca	1134d
OY	1401	gtatcaagcgtgaagctaaagattctgtgaagagatacttctgaacaaagatcacccgcaaa	1460m
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OY	1481	atgagccgtgttcaagaacgtactcaactccttctgtgtgcgagatgaacaaagagaatcccg	1520m
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OY	2001	tttctcgttgattacaactttttacatgtgtcacaataaagggtctcaatatacaagcgg	2060m

D6	1735	TTTTCTGGGTTACCAAAATTTTGCACGGGTGCAGATCGGGGGTTCAATTACAAGACCA	1794
OY	2061	cattaaagcatttcgcaaaaagaatgatctcttctccctaattttaaacgcgtcat	2120
D6	1795	CACATAAAGAGATGCAAAACTGATGTGGCTTTTAATTGGAGCCGT-----CATCGAT	1846
OY	2121	tatgtgaaccctgaattgatagtttccccct-----cctgtcccataccctctgltcaatagt	2175
D6	1847	TATATGGGCCCTAATTGGCTGTGTACCTCCTGGCCCTGGCCCTGCCCCCTGAAGCTGGTCA	1906
OY	2176	alcattatctctgttcogtgctgcgtcgctgttgtaacatagaattttgtfagaagaata	2235
D6	1907	ATGACCATTCCTGTTTGTTGATGC-CCCTGCCCTGTGGCCGTGTAAGCTTTTGTAGAAGTA	1965
OY	2236	catgtaaaaatcttttgtlaatg--aatcgaalgaabagtgttcttaagaanaatatagtg	2292
D6	1966	CATGTAAGAATCCTGTGTAATGGCGAANAATCATGTGTTTGTCAAGAAAATATATAGTGTCA	2025
OY	2293	catgttgtctctttttgtcccaagtaa	2317
D6	2026	TTTTGTTCTTTTNTTGGCTCGCTAA	2050

RESULT	3
LOCUS	MZECDPKB
DEFINITION	2228 bp mRNA PLN 06-FEB-1999
ACCESSION	U000000000
KEYWORDS	zea mays mRNA for CDPK-related protein kinase, complete cds, clone zmcCRK3.
SOURCE	DB4508
ORGANISM	DB4508.1 GI:1313908
REFERENCE	CDPK-related protein kinase; calcium-dependent protein kinase-related kinase; CRK.
AUTHORS	zea mays (strain:lnbred line H84) Root CDNA to mRNA, clone_11b:lambda gt10 clone:zmcCRK3.
TITLE	zea mays
JOURNAL	Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC Clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 2228)
TITLE	Furumoto, T., Ogawa, N., Hata, S. and Izui, K.
JOURNAL	Direct Submission
AUTHORS	Submitted (27-APR-1996) to the DDBJ/EMBL/Genbank databases.
TITLE	Tsuyoshi Furumoto, Kyoto University, Graduate School of Agriculture Lab. of Plant Physiology, Sakyo-ku, Kyoto, Kyoto 606-01, Japan (E-mail: tsuyo@kais.kyoto-u.ac.jp, Tel: 075-753-6142, Fax: 075-753-6146)
JOURNAL	2 (sites)
AUTHORS	Furumoto, T., Ogawa, N., Hata, S. and Izui, K.
TITLE	Plant calcium-dependent protein kinase-related kinases (CRKs) do not require calcium for their activities
JOURNAL	FEBS Lett. 396 (2-3), 147-151 (1996)
MEDLINE	97072168
FEATURES	Location/Qualifiers
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	/evidence=experimental
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RESULT	4
D38452	D38452 1784 bp mRNA PLN 27-SEP-1997
LOCUS	
DEFINITION	zea mays mRNA for calcium-dependent protein kinase-related kinase, partial cds.
ACCESSION	D38452.1 GI:2443387
VERSION	
KEYWORDS	calcium-dependent protein kinase-related kinase.
SOURCE	zea mays (strain:Inbred line H84, haplotype:2) Seedling Leaf cDNA
ORGANISM	zea mays
REFERENCE	Eukaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta; Magnoliophyta: Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 1784)
TITLE	Izui, K.
JOURNAL	Direct Submission
REFERENCE	Submitted (01-OCT-1994) to the DDBJ/EMBL/GenBank databases. Katsura
AUTHORS	Izui, Kyoto University, Agricultural Biology; Otake-cho,
TITLE	Kitaohikakawa, Sakyo-Ku, Kyoto, Kyoto 606-01, Japan
JOURNAL	(tel:075-753-6140, fax:075-753-6146)
REFERENCE	2 (sites)
AUTHORS	Furumoto, T., Ogawa, N., Hata, S. and Izui, K.
TITLE	Plant calcium-dependent protein kinase-related kinases (CRKs) do not require calcium for their activities
JOURNAL	FEBS Lett. 396 (2-3), 147-151 (1996)
MEDLINE	97072168
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	/codon_start=1
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	RADNFDGSPWPSVSAEKDFVKRFLEKDYRKMTAVQALTHPMLRDEORQIDPLLI
	FRLLKQYLRTPLKRLALKLSLSDLELTYRLQKLLPEPDGVSIDNFRATLR
	YSTDAHRESVLEFOHALERLPLATYRKMDPEECCAALISPVQLELREWEETAGTAPDH
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	RH"
BASE COUNT	478 a 368 c 431 g 507 t
ORIGIN	
Query Match	47.7%; Score 1133; DB 8; Length 1784;
Best Local Similarity	83.5%; Pred. No. 1.3e-161;
Matches 1353; Conservative	0; Mismatches 245; Indels 23; Gaps 5;
Y	708 tacgagctccggaagaagagtgaggagggccacttcggaacacacttgctccgctgcgtc 767
Db	1 TACGATCTCGGGAAGAGAGTGGGAGGGGCCACTTTGGCCACACACTCTCCGCGCTGTC 60
Y	768 aagaagggcgagtaacaaggacagaccgttcgctgaagatcactcgcgaagctaagatg 827
Db	61 AAGAAAGGCGCGACCAAGGGCCATACCGTGCCTCAAGATCATCTCCAAGCTAAGATG 120
Y	828 acaacggcaatcatcttgagatgtctcgtagaagaataaatttttgagagcgttatcc 887
Db	121 ACAACGGCCATTTCCATTTGAAGATGTTGTAAGGAGAGTCAAGATTTTGAAGCCCTTTCA 180
Y	888 ggagcaataatcttcgcgaataattctatgatcagtgtgaagatggcctcaatgcttcaatt 947

Db	181	GGGCAACGTAATATCTCGTACAAATTCATGATGCAATGTGAGAGCCCTCAATGCTACATT	240
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Db	241	GTCATGCAATTAATGTGAAGGTGGAGATTGCTAGACAGAAATTTTACGAAGAGTGGGAGA	300
Qy	1008	taccagaagaagatgcaccaagcatctgtctacagattctgacgtagtagcctctct	1060
Db	301	TATACAAAGAAATGCGCAAGCGAATCTTGACAGATTTTTCAGATGCGTGTGGCTTCGT	360
Qy	1068	cattcgaagggttagtgcacgtctgatttgaaagccaaggaattcctcttcaaccaagg	1120
Db	361	CATTTTAAAGGAGTACTGCACTGCTGATTTGAAGCCAGAGAAATTTCTTTCACAAACAGA	420
Qy	1128	gatgaaatgctcccaatgaaatgtatgtaatttggtctctctgattcattacagcat	1188
Db	421	GATGAAAGCCCTCTATGAAAGTTGATTCACCTTGGCTGTGAGATTTTATTAAGACAGAT	480
Qy	1188	gaaagccttaataatattcttgaaagtgatatttctgtgccagaggtttacaaga	1248
Db	481	GAAGGCTCATATATATTGTTGGAAGTGTATTAATTAATGTTGCTCCAGAGGTTCTACACAGA	540
Qy	1248	tcatatagiatggaagcacacattggaatagatgtagtgcataacgtatcgtctgt	1308
Db	541	TCATACAGTATGGAACACACATTTTGGAGTATAGGTATTAATACATATTCTCTCTGT	600
Qy	1308	ggacgctcgccacatctcgggacagaaacacagaataatccgactctgtgtgagaat	1368
Db	601	GGCAGTCGCCATTTCTGGGCAAGACAAATCTGGATCTTCCGCTCGATTAAGAGGCT	660
Qy	1368	galtcccaactttgatgatctcacccgctgagcctacagatcacgtgaagctaaagatttg	1428
Db	661	GATCCCAATTTTGAAGGTTACACCAAGGCTTCACATTCGGCTGAGGCTTAAGATTTTGTG	720
Qy	1428	aagagatctctgaacaaagattaccgcaaaagaaatgacgcgtgttcaagcactgcat	1488
Db	721	AAGAGATTTTCTAACAAAGATTACCGGCAAAAGATGACTGCTGCCAAGCAGTACGCTAC	780
Qy	1488	ccttggttcgagatggaacaaagcagatcccgcttggaactactcatcttcagattaat	1548
Db	781	CCTTGGTTACGAGATGACAAAGGCAATTTCAATTGACATACATTTCACATTGATT	840
Qy	1548	aagcaatactccgcgtcacacctcttaaacggtctgagcatlaaaggcaataccaagct	1608
Db	841	AAGCAGTATCTCCGCTACTCTCTTAAACGTTTGCAATTAAAGGACATCTAAGCT	900
Qy	1608	ttaagggaagatgaaacttttgaactcaaacactgcaagttaaacctgctgaactagat	1668
Db	901	TTAACGAGATGAACTTTTATCTTAGTGTGCAAGTTAAAGTGTTAACCCAGAT	960
Qy	1668	gggcttgcatactgacaactcttcgagcgacataagcgtacatctaacatgactgata	1728
Db	961	GGGTTCCGTCACTCGCAACATTTTCGAGCGCTGTGCAAGATACCTCACTACGCCATG	1020
Qy	1728	aaggaatcgagagttcttgaaattttgcatagcttggaacacttgcatacagaagat	1788
Db	1021	AGAGATTAAGGGTCTTGAGTTTCACCACTGCTTGGAACCACTTGCCTGACAGAAAGATG	1080
Qy	1788	gacttgaaggtctctgcccagacatagcccttaacagcttgaagcacttggaag	1848
Db	1081	GACTTGAAGAAATCTGTGCTGCAGCAATCAGCCCTACCACTGGAAGCTTTGGAAGG	1140
Qy	1848	tgggaagagatctgtgaaacagcttccagcaattgaaacagaggcaaccgagtcata	1908
Db	1141	TGGGAAGAAATTCGTGGAAACAGGTTTTCAGCACTTTCGAACAAGAGGCAACCGATATTATA	1200
Qy	1908	tcagctgaaggaatgaacaggaatlaaatctgtgcccaaacctattaccatcagtcgtaa	1968
Db	1201	TCAATTGAGGAGTTAGACACAGAACTTAATCTCGCCGCACACATTAATCCCAATGTGTGAA	1260
Qy	1968	gactgatacgaaaatccgattgccaagactaaactctcgtggttttacaanaatttacaat	2028

Db	1261	GACTGATTCAGAAATAATCGAGCGCAGCTTAACCTTCTTGSTTTCACCAAAATTTTGGAC	1320
Qy	2028	ggtgtcaacaataagggtctcaaatacaaagcggcatlaagcgaattgtcaaaagaanaatg	2087
Db	1321	GGTGTACAGATACGGGGTCTCAAAATACAAAGACACACTAAACAGATGCAA-----	1369
Qy	2088	attctttctctcttaattttaagc---cgctcaatlaagtgaccctgattgattcttc	2144
Db	1370	ACTGTATATCGCTCTTAATTAAATGGAAGCCCTCTCAGCATGATTAACGGCCCTAATGCTGTATCC	1429
Qy	2145	cccc-----ccgtgcctcaatccctcgtgcgaatagatcatattctgttcgtagctg	2199
Db	1430	TCTCGCTGGCGCTGGCCCTGGCCCTCAGTCTGGTCAATGACCATCTTGTTTGTAATGC-	1488
Qy	2200	gtcggcgtgtgtcatcatagtttctgttagaagaatacatgtaagaatccttgttaatg--	2257
Db	1489	CCCTCCGGCTGTTGGCGTGTACTCTTTGTAGAGTACATGTAATAATCCTTGTAATGCG	1548
Qy	2258	-aatcgaaatgatatglttgtgtccaagaatatagtgatcagtgtgtctcttltttgcccagta	2316
Db	1549	AAATCATATGTTTGTGCTCAGAAATATATAGTGTATTGTTCTTTTGTGGCTGCCTA	1608
Qy	2317	a 2317	
Db	1609	A 1609	

RESULT	5			
LOCUS	AF009337			
DEFINITION	AF009337	1562 bp	mRNA	PLN 01-JUL-1998
ACCESSION	Tradescantia virginiana CDPK-related protein kinase (CRK1) mRNA,			
VERSION	partial cds.			
KEYWORDS	AF009337			
SOURCE	AF009337.1	GI:3282249		
ORGANISM	Virginia spiderwort.			
	Tradescantia virginiana			
	Euphorbia Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; Liliopsida; Commelinales;			
	Commelinaceae; Tradescantia.			
REFERENCE	1 (bases 1 to 1562)			
AUTHORS	Sukanya, R. and Wolniak, S. M.			
TITLE	A CRK like sequence from Tradescantia virginiana			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 1562)			
AUTHORS	Sukanya, R. and Wolniak, S. M.			
TITLE	Direct Submission			
JOURNAL	Submitted (18-JUN-1997) Plant Biology, University of Maryland, H.J			
FEATURES	Paterson Hall, College Park, MD 20742, USA			
source	1. .1562			
	Location/Qualifiers			

gene
CDS

474 a 287 c 336 g 465 t

BASE COUNT
ORIGIN

	Query Match	Similarity	Score	736.2	DB 8	Length	1562
	Best Local	Similarity	76.5%	Pred	1.2e-101		
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Qy	886	caaggacacataatctcgtctaaatttctatgtagcatgtgagaatgcttcaatgtctctaca	945				
Db	61	ctggctcattaaacatcttggtaaaattctatgtagcattgtagaagatcccttaattgcttacc	120				
Qy	946	ttgcctgtagaattatgtgaaaggagagaattctctagacagaatctatgacagaacgagcgga	1005				
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Qy	1006	gatacacagagaagaatgacacgaatgtgtgtagacagattttagacgtagagcctctc	1065				
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Qy	1066	gtacatctcgaaggagtagtgtagcatgtagatttgaagcagaagaattctcttccaaacaa	1125				
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Qy	1126	ggagtagaanaatgctcccatbgaatgtgattgatttgcctcctgattcatttagaacag	1185				
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Qy	1186	atgaaagagcttaatgatatgttctggaagagagcatatgatttgcctccagaaggtttaaaca	1245				
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Qy	1246	gatacatagatatgaaagcagacatttggagtagatgtagtctcaaaagctaacattcgcctc	1305				
Db	421	gatacatagatatgaaagcagacatttggagtagatgtagtctcaaaagctaacattcgcctc	480				
Qy	1306	gtggcagctcgagcgaatctctgggacgaacagaatcaagaatattccagatctglttgagag	1365				
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Qy	1366	ctgtgctccaaattttagatgattacacgctgggacgaatcaagaatattccagatctglttgagag	1425				
Db	541	ctgtgctccaaattttagatgattacacgctgggacgaatcaagaatattccagatctglttgagag	600				
Qy	1426	tgaagagatcttctgaacaaagaattaccgcgaacaaagaatgaacgctgttcaagacagctac	1485				
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Qy	1486	atcccttggttgagagatgtaacaaagcagatcccgctgtgacatactcatctccagattaa	1545				
Db	661	atcccttggttgagagatgtaacaaagcagatcccgctgtgacatactcatctccagattaa	720				
Qy	1546	ttaagcaatccctccgagctacacccctttaaagcgtgttgactaaagagacatacccaag	1605				
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Qy	1723	ctaaagaaagaaatcgagggtcttctgaaatttctgcatgcgttggacaaactctcatcacaga	1782				
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Qy	1783	gaatgagcttgaagagttctgtgctgcgacgaatcaagctccattaccagcttgaagcactg	1842				
Db	961	gaatgagcttgaagagttctgtgctgcgacgaatcaagctccattaccagcttgaagcactg	1020				

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Qy	1903	lcatatcagttcgaagactaacacagagacttaaacctgtccccaactcattatccacgcg	1962
Db	1081	TGCTCTCAGTTGAGAACTTACACACAGGATTGTAACCTTCCCTCAGATCCCTATGCAATTC	1140
Qy	1963	ttcaagactgcatcagaataatccgattgccaagttaaaccttccggtgttaccacaaat	2019
Db	1141	TTAAAGATTGGATTAGACAGTCAGACAGAAAGAGCTGAGTTTCTCGGATACACTGAT	1197
RESULT	6		
LOCUS	DCCRK	2146 bp	MRNA
DEFINITION	D. carota mRNA for CDPK-related protein kinase.		PLN
ACCESSION	X83869		04-DEC-1995
VERSION	X83869.1	GI:1103385	
KEYWORDS	calcium-dependent protein kinase; crk gene; PK421 gene; protein kinase.		
SOURCE	carrot.		
ORGANISM	Daucus carota		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Apiales; Apiales; Daucus.		
AUTHORS	1 (bases 1 to 2146) Lindzen, E. and Choi, J. H.		
TITLE	A carrot cDNA encoding an atypical protein kinase homologous to plant calcium-dependent protein kinases		
JOURNAL	Plant Mol. Biol. 28 (5), 785-797 (1995)		
MEDLINE	95367641		
REFERENCE	2 (bases 1 to 2146) Choi, J. H.		
AUTHORS	Direct Submission		
TITLE	Submitted (12-JAN-1995) J. H. Choi, School of Biology, Georgia		
JOURNAL	Institute of Technology, Atlanta, GA 30332, USA		
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 KEYWORDS thale cress.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis
 1 (bases 1 to 2005)
 AUTHORS
 Choi,J.H. and Lala,H.
 CDPK-related kinases in Arabidopsis
 unpublished
 2 (bases 1 to 2005)
 REFERENCES
 Choi,J.H. and Lala,H.
 Direct Submission
 Submitted (21-MAY-1999) School of Biology, Georgia Institute of
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 TITLE
 JOURNAL

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 AF153351.1
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE
 1 (bases 1 to 2148)
 AUTHOR
 Choi, J.H. and Lala, H.
 TITLE
 CDPK-related kinases in Arabidopsis
 JOURNAL
 Unpublished
 2 (bases 1 to 2148)
 REFERENCE
 Choi, J.H. and Lala, H.
 AUTHORS
 Direct Submission
 TITLE
 Submitted (21-MAY-1999) School of Biology, Georgia Institute of
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 Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
 Oryza.
 REFERENCE 1 (Bases 1 to 1828)
 AUTHORS Cheong Y.H., Moon,B.C. and Cho,M.J.
 TITLE Isolation of calcium-dependent protein kinases from rice
 JOURNAL unpublished
 REFERENCE 2 (Bases 1 to 1828)
 AUTHORS Cheong,Y.H., Moon,B.C. and Cho,M.J.
 TITLE Direct Submission
 JOURNAL Submitted (13-OCT-1999) Biochemistry, Gyeongsang National
 University, Gwaza dong, Chinyu, Kyungnam 660-701, Korea
 3 (Bases 1 to 1828)
 AUTHORS Cheong,Y.H., Moon,B.C. and Cho,M.J.
 TITLE Direct Submission
 JOURNAL Submitted (29-JAN-2001) Biochemistry, Gyeongsang National
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VERSION
AF289237.1 GI:9858872
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
1 (bases 1 to 7359)
Lu, Y.-T., Liang, S. and Wang, L.
Cloning of a calcium/calmodulin-dependent protein kinase gene, MCK2
from maize
Unpublished
2 (bases 1 to 7359)
Lu, Y.-T., Liang, S. and Wang, L.
Direct Submission
Submitted (25-JUN-2000) Center for Developmental Biology, College
of Life Sciences, Wuhan University, Wuhan, Hubei 430072,
China

FEATURES
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VERSION AX077711.1 GI:13122086
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REFERENCE Holt,C.D., White,A.J., Michael,A.J. and Osborn,R.W.
AUTHORS Herbicide resistant plants and methods for the production thereof
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JOURNAL ZENECA LIMITED (GB)
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GenCore version 4.5
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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8	239.2	10.1	1761	21	Arabidopsis thaliana
9	233.6	9.8	1836	21	Arabidopsis thaliana
10	233.2	9.8	1647	22	Liverwort calcium
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12	229.4	9.7	2040	22	AAE74278	Rice calcium depen
13	224.2	9.4	1791	22	AAE74270	Carrot calcium dep
14	220.6	9.3	1392	21	AAE48741	Arabidopsis thaliana
15	219.8	9.3	1020	19	AAV36878	Nucleotide sequenc
16	217	9.1	1723	22	AAE74271	Maize calcium depe
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19	213.8	9.0	2306	22	AAE74272	Maize calcium depe
20	212.8	9.0	2550	22	AAE74283	Cucurbita pepo cal
21	211.2	8.9	2436	22	AAE74273	Soybean calcium de
22	209.8	8.8	2334	22	AAE74277	Rice calcium depen
23	208.2	8.8	1506	21	AAE74287	Arabidopsis thaliana
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27	205.6	8.7	1910	22	AAE74275	Sweet potato calci
28	203	8.6	1726	22	AAE74263	Arabidopsis calciu
29	194.8	8.2	2087	22	AAE74266	Arabidopsis calciu
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32	174.2	7.3	2466	15	AAE6397	Protein kinase cDN
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38	126.8	5.3	1412	21	AAE51681	Zea mays DNA fragm
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DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 68642.
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XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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PR 18-OCT-1999; 9905-0159584.
PR 21-OCT-1999; 9905-0160741.
PR 21-OCT-1999; 9905-0160767.
PR 21-OCT-1999; 9905-0160768.
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PR 22-OCT-1999; 9905-0160981.
PR 22-OCT-1999; 9905-0160989.
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PR 25-OCT-1999; 9905-0161406.
PR 26-OCT-1999; 9905-0161359.
PR 26-OCT-1999; 9905-0161360.

PR 26-OCT-1999; 9905-0161361.
PR 28-OCT-1999; 9905-0161920.
PR 28-OCT-1999; 9905-0161992.
PR 28-OCT-1999; 9905-0161993.
PR 29-OCT-1999; 9905-0162142.

Query Match 22.5%; Score 533; DB 21; Length 1309;
Best Local Similarity 67.8%; Pred. No. 1,7e-99;
Matches 746; Conservative 0; Mismatches 355; Indels 0; Gaps 0;

QY 958 tatgtgaggagaagaattgtctagacagaatatagccagagcgaggagataacagagg 1017
DB 1 tatgcgaaggtgagagcatalgtgatatgaatttggcgagaggtgagcagatccctgaag 60
QY 1018 aagatgccaaagcgatgtgtacagattttagcgcgtgagtcgcttcgtcatctcagg 1077
DB 61 tcgatgccaaacgtatctctgtgcagatttgtctgcgaacgcatttctacacccaag 120
QY 1078 gggtagtcacatcgtgattttagagccagagaatttccttccacacacaggaatgaaatg 1137
DB 121 gtgtcgtgcacccgtgacatcgtagagccgagaaatttccttccacagagaatagagatg 180
QY 1138 ctcccatgaagtgtatgtatttgcctcctgattcattatagaccagatgaaagctta 1197
DB 181 cgatacccaaggtcatagatttgtcctgtctgtattcatatagatacagatcagcttca 240
QY 1198 atgatattgttggagatgcataatattgtgcccagaggtttacagatcatatagta 1257
DB 241 atgatatgttggagagtcataacatcgtgcacatgcagatccccaatagatccttaccga 300
QY 1258 tggagagcaaacatttggagtaagtgatcacaacgtacatctgtctgtgcagtcggc 1317
DB 301 ctgagagcagatatgtgagacatcgtgtcatatagttacatacttcctcgtggaagcagac 360
QY 1318 catctgtggcagcagcaagaatcaagaatatccgattcgtgtttagagctatcccaact 1377
DB 361 ctctctatggagaagcctgagcttgcataatcctgtctgtgttgcataacacccaatt 420
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DB 421 ttgagatatgtccttgcctctctatctcctacatgcacaaagacttcgtgaaagcttt 480
QY 1438 tgaacaagaattacccgcaaaagaatgacccgtgttcaagcactcatccttctgttgc 1497
DB 481 tgaacaagaccataggaacgaatgacagctgttcaagcctcatcgtcatcgcgtttac 540
QY 1498 gagatgacaagaagcagatcccgctgtgacatccatcttcaagtaattcaagaatcc 1557
DB 541 gtgacgaaaaccccggtttgtcttcttattctcgttcatcaagttgttcaagctcta 600
QY 1558 tcgcgcgtacacactcttaaaagcttggcattaagggcactatccaaagccttaagggaag 1617
DB 601 tcgctgcctcacacttcccgacatcagaacttaagctctctcgtgaaagcttaccctgatg 660
QY 1618 atgaacttgttatctcaaacatgcagtttaaacctgtcgaacccttagagatggtttgat 1677
DB 661 aagaactgtgtctccttaagcagatgcagttcagctcccttgatccctaaagaagagccat 720
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DB 781 ggcttccgtacattttaatcagatgcacactctggcgcaaaaagacttgaactttagag 840
QY 1798 agttctgtccgcagcaatcagctccttaacagccttgaagcacttgaaggttggagagga 1857
DB 841 agttctgtgcgctgcgctcagttcagtttcaacaactgagagccttgaagaatcggaacaga 900
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PR 17-AUG-1999; 99US-0149175.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 16-SEP-1999; 99US-0154039.
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PR 28-SEP-1999; 99US-0156458.
PR 28-SEP-1999; 99US-0156586.
PR 04-OCT-1999; 99US-0157117.
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PR 06-OCT-1999; 99US-0157865.
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PR 08-OCT-1999; 99US-0158232.
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PR 29-OCT-1999; 99US-0162142.

Query Match 10.8%; Score 255.8; DB 21; Length 1671;

Best Local Similarity 52.8%; Pred. No. 5.3e-43;

Matches 635; Conservative 0; Mismatches 547; Indels 21; Gaps 3;

QY 797 cgcgcgaacatcatcgcaagctaagatgacacgcaatcatccatctgagatctcg 896
DB 369 cgctgtgaagtcataatccacaagagaagtgtgactcttaagaagaagtgtcgagatctgag 428

QY 857 tagagaagtaaaaaatttgagaagcgttatacaggcacataatctcgtcaattctatga 916
DB 429 aaggagaattcagataatgcatlctatgctgtcagcaggtatctcgtacgatataagg 488
QY 917 tgcattgagagatggccccaatgctcatcatctgcatgtaattatctgaggagagaatt 976
DB 489 agcttatgagaacctcttgatgttcatcatggttcatggaagcttctgtctgaggtgatt 548
QY 977 gctagacagaaltatagccaagagcgagatatcacagaagaatgccaagcgattgt 1036
DB 549 gttcgatagattatccagaga---gacattatagtagaggaagcgtctgagctgac 605
QY 1037 tgtacagatttggcgcgtagagccttctgtcatcttcuaggggtgagctgtgatt 1096
DB 606 taagatcatctgctgtgttcttgaagcgtgcatcctgtgtgtgataagagact 665
QY 1097 gaagcagaagaatttcccttcacacacagagatgaanaatcctccatgaagttgatga 1156
DB 666 gaagcctgagaattctctatgttataagaagatgattctctcctcaagcctatga 725
QY 1157 ttctgtctctctgatttcaatagacagatgaagccttaatgatatgttggaaagtgc 1216
DB 726 ttctggctcatctgtcttcttcaaacagagtcacaatatctcatgtgttggaaagctc 785
QY 1217 atattatgtgccccagaggtttacacagatcatatagtatggaaagacatttgag 1276
DB 786 atattatgtgtctcctctgaggttctgccaacagttatggcctgaagcgtatgtgtgagc 845
QY 1277 tataggtgtcaaaagtlacatctctgtctgtgagcagtcgcacattctggagcaacaga 1336
DB 846 tgcgtgtgtatattgtatataatctgtaaacgaggtccacactcttggagagaacaca 905
QY 1337 atcaggaatttccagatcgtgtgagagcgtatcccaactttgatattacacgtgtgc 1396
DB 906 gcaagggatattctgactgtctgttgaagaagatatatgcacttgaatcagaccgtgtgc 965
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DB 966 tgtgatatcgcagacagtgctaaagcctgtatccgagaaatgtatccccaagccttgaga 1025
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DB 1026 acgtttgaccgctatgaaatctgtgcgtatccatcgtatcgtatgaaatgtgtgcacc 1085
QY 1511 gcaagatccgctgtaacatccatcctcagatataatgaagaatacctcgcgtacaacc 1570
DB 1086 agatagagcactagatccaaagctgttcttctgtcttcaagaatctcttgcataatga 1145
QY 1571 tcttaaacggttgcattaaagcactatccaaagcctttaaaggagaatgaactttgta 1630
DB 1146 actaaagaagaatggtcttgaaggtatagcgtgagagcctctcggaaagaagatagcttg 1205
QY 1631 tctcaaacctcagtttaaacctgtcgaacctagagatgaggttgcatacacttgaacact 1690
DB 1206 tttaagaagaatgtttaaagcaatggaatctgataaacaagcggtgaatccatltgtga 1265
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DB 1326 tatgtagtgcgcgtagttagacaacagtgtagacaatagatatacagtgagttcatltgagc 1385
QY 1811 agcaatcagtccttaccagcttaggcactcgtgaaggttggagagagatctcgtgaacagc 1870
DB 1386 gacgatccatctcaacaaactaga-----gcgggaagagcatcttcttgagc 1433
QY 1871 ttccagcaatttgaacaagaagcgcaacgcagcatcatctgtagaagaatttagcaagga 1930
DB 1434 gttcataatatttgcacaagaatggaagcgttcttcaatacaatgtatgagctacaacaagc 1493


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OY 1931 attaaattgtctccaactcatctaccatcgttcaagactgatacgaataatccgatg 1990
DB 1494 gtgtgttgacaatgcatgcatggtgtgtttcttcttgaaagacatcatcaagaattgatca 1553
OY 1991 caa 1993
DB 1554 aaa 1556

RESULT 7
AAF74276
ID AAF74276 standard; DNA; 2251 BP.
XX
XX AAF74276;
AC
XX
XX 04-MAY-2001 (first entry)
DT
XX
DE Tobacco calcium dependent protein kinase clone.
XX
XX Calcium dependent protein kinase; CDPK; herbicide resistance;
XX paraquat; diquat; crop production; ds.
XX
XX Nicotiana tobaccum.
OS
XX WO200107592-A2.
XX
XX 01-FEB-2001.
PD
XX 26-JUL-2000; 2000WO-GB02876.
PF
XX 27-JUL-1999; 99GB-0017642.
PR
XX
XX (ZENE) ZENECA LTD.
PA
XX Holt CD, White AJ, Michael AJ, Osborn RW;
PI
XX WPI; 2001-168549/17.
XX
XX Producing herbicide resistance plants by inhibiting calcium dependent
XX protein kinase in plants or by providing an intracellular vacuolar
XX transporter capable of transporting agrochemical into plant vacuole -
XX
XX Claim 18; Page 38-39; 50pp; English.
XX
XX The present invention describes a method of producing plants which are
XX resistant to the herbicides paraquat and diquat, involving inhibiting in
XX the plants a calcium dependent protein kinase (CDPK) and selecting those
XX plants which are resistant to the agrochemical of interest. This is
XX useful in the production of crops with herbicide resistance.
XX
XX Sequence 2251 BP; 743 A; 371 C; 537 G; 598 T; 2 other;

Query Match 10.2%; Score 243.2; DB 22; Length 2251;
Best Local Similarity 54.2%; Pred. No. 2.1e-40;
Matches 538; Conservative 0; Mismatches 448; Indels 6; Gaps 2;
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OY 1086 catcgtgatttgaagccagagaatttccctttcaaacccaggatgaaatgctccatg 1145
DB 813 catagggtatttaagccagagaatttcttactagtaagatgaaatgcaagctc 872
OY 1146 aagttgatttggctctcgtatctcatttagaccagatgaaggtcaatagatatt 1205
DB 873 aaggcaaccgattcttgaccttcgtctctcatcgaagaagggaaggtgtaccgggata 932
OY 1206 gttggaatcatattatgttgcctccagagatttttaacagatcatatagatgaaga 1265
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DB 1053 gctgaacttgaaagggaattatcattgcatctaaagggaatgtgacttcaagt 1112
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OY 1446 gattaccgcaaaagaatgacccgtgttcaagcactgacatccctgtgtgcga--gat 1502
DB 1173 gagccaaaggagaagagatgacttcagacaaagttcttgaaactcatgtgttcgaatgga 1232
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OY 1623 ctgtgtatctcaaacctgcagctttaaactgtctcgaacctgaagatggtgttactct 1682
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OY 1683 gacacttgcgagcactaagcgatatttaactatgtctatgaaggaatcgaaggtt 1742
DB 1413 tatgaagaattgaaagtcggaattgctcgtcttgatcaaaagctaaagagaccgaagtc 1472
OY 1743 ctggaatttgcagctgttggaaccacttcgacatacagaagaatggaagcttgaagctt 1802
DB 1473 aagcaactcatggaagctgtgtgatagtgaggaatggaacatcgactacatcgagtt 1532
OY 1803 tgtgcgcgaagaatcagctccttacaagcttga 1834
DB 1533 attactgcacaacatgcatagacatcggttga 1564

RESULT 8
AAC42353
ID AAC42353 standard; DNA; 1761 BP.
XX
XX AAC42353;
AC
XX
XX 17-OCT-2000 (first entry)
DT
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 35231.
DE
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
OS
XX EP1033405-A2.
XX
XX 06-SEP-2000.
PD
XX
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PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
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RESULT 11

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 ID AAF74282 standard; DNA: 1647 BP.

AC AAF74282;

DT 04-MAY-2001 (first entry)

DE Liverwort calcium dependent protein kinase clone #2.

KW Calcium dependent protein kinase; CDPK; herbicide resistance;

KW paraquat; diquat; crop production; ds.

OS Marchantia polymorpha.

PN MO200107592-A2.

PD 01-FEB-2001.

PE 26-JUL-2000; 2000MO-GB02876.

PR 27-JUL-1999; 99GB-0017642.

PA (ZENE) ZENCA LTD.

PI Holt CD, White AJ, Michael AJ, Osborn RW;

DR WPI; 2001-168549/17.

PT Producing herbicide resistance plants by inhibiting calcium dependent
 protein kinase in plants or by providing an intracellular vacuolar
 transporter capable of transporting agrochemical into plant vacuole

PS Claim 18; Page 42; 50pp; English.

CC The present invention describes a method of producing plants which are
 CC resistant to the herbicides paraquat and diquat, involving inhibiting in
 CC the plants a calcium dependent protein kinase (CDPK) and selecting those
 CC plants which are resistant to the agrochemical of interest. This is
 CC useful in the production of crops with herbicide resistance.

SO Sequence 1647 BP; 445 A; 348 C; 464 G; 390 T; 0 other:

Query Match 9.8%; Score 233.2; DB 22; Length 1647;
 Best Local Similarity 55.7%; Pred. No. 2,1e-38;
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 QY 891 cacaaataatcgtcacaattctatagatgcatgttagagatgucctcaatgtctaatgttc 950
 Db 415 cagaagaacatctgtcgatttgaaggggccctatgaggatataacccaacgcgtcatctgctc 474
 QY 951 atggaatatagtgagggaggaagaaatgtctcagacaaataltagccagaagcgaggatgac 1010
 Db 475 atggaagcttgtgtgtgctgaggaacactctcagccgcatatttcagcgggc---cactac 531
 QY 1011 acagaagaaatgccaagcgatgtgtgtcagatttggcgtgagtagagcctctgtcat 1070
 Db 532 agtgaagagggctgctgcagcctctatgttagaactatagtcagaagtggttcagacgttcat 591
 QY 1071 ctccaaggggtagtgacatcgtagatttgaagccaagaaatttcccttccacaacagagat 1130
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 QY 1131 gaaaatgctcccatgaaagtgtgatttgcgtctcgtatctcatatgaccagatgaa 1190
 Db 652 gaggatgcacccctgaaagcgacggaatttgcgtcttcttctctcctcaagccttgagaa 711
 QY 1191 agccttaatgatatgttgaaatgcatatattgttgcacagaggttttacaagaatca 1250
 Db 712 gtgtttacagatatcgtttgaagtgcttaactaagctgagcaacaaggtttgcgtctaac 771
 QY 1251 tatagtatggaagcagacatttggagatagtgctcaataacgtacattctgctctgtgac 1310
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 QY 1311 agtcggccattcggcgacagacagaatcaggaatattccagatctgtgttgagagctgat 1370
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 Db 892 atgatttcaatagtgatccttgccttcaattctcacaagcgaaagtcgtgtaag 951
 QY 1431 agatttctgacaacaaatattccgcaaaagaaatgaacgcgtgttaagacactgactactct 1490
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 QY 1491 tggctgcagatgaacaaag-----cagatccgcgtcgacatactcattcctaagatta 1544
 Db 1012 tggatttagtggttgcagcgagagcgaccagacaacacacttgacaagcggtgtgtctaga 1071
 QY 1545 attaaagcaatcctccgcgtctacacctctttaaacygttgcgtatlaaagcaactatccaag 1604
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RESULT 12

AAF74278
 ID AAF74278 standard; DNA: 2040 BP.

AC AAF74278;

DT 04-MAY-2001 (first entry)

DE Rice calcium dependent protein kinase clone #2.

KW Calcium dependent protein kinase; CDPK; herbicide resistance;

KW paraquat; diquat; crop production; ds.

Db 638 gctacgattctgtagcgagatttggaattgtgcaatgcttgcattgttgcattttagtggtggatcg 697
Oy 1086 catcgagatttgaagccagaagaatttccttcttcaacaacgaggaatgaatgtcccaatg 1145
Db 698 catagagattcttaagcttgaataattctctgtcttcgagtaaggaatgaatgcaatgctg 757
Oy 1146 aagttgattgatttgcctctctgattcattatagaccagatgaagagcttaattgattt 1205
Db 758 aagggcagcagatttgcgtgtactctgtcttccattggaagaaggaagtatactgtaata 817
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Db 878 gatattcgagcgtctggaatttcttctatatactactacgagggttacctcattcttg 937
Oy 1326 gcaagacagaatcagaatattccgattctgtgtgagagctgaccccaattctgattg 1385
Db 938 gcaaggaatgaaataaggaattatttgaatgcaatactggaagagtgattgacttgaagt 997
Oy 1386 tcaacgctgagcctacagatcagctgaagctgaagatttgtgaaagagattcttgaacaa 1445
Db 998 gaaccatggtcactcagctccaaacagtgcaaaagacctgtgtaagaagatgctgacacag 1057
Oy 1446 gattacccgaaagaatgagccgtctgttcaagacagctgacatccattctgttgcagat 1502
Db 1058 gatccaaaggaagaagatttactctctgcacaagttcttgcacatccctgagatgagaag 1117
Oy 1503 ---gaacaaaggcagatcccgctgagacatactcattcagatlaaataagcaataccctc 1559
Db 1118 ggaagaagcatcagacaagcaatagatgtagtcagctctctctgaagtgaagcagttccag 1177
Oy 1560 cggcgctaccccttaaacggttgcataaaggcacttccaaggctttaaagggaagat 1619
Db 1178 gcaatgaacaagctcaaaacacttgcacttaaggtcattcgttgaagctcattccgagaa 1237
Oy 1620 gaacttctgattcacaactgtcagtttaactgtcgaactggaacctgagatgttgcata 1679
Db 1238 gaataataaggtcttaataaccatggttgcacaacatggaacaggaacaaagtgttacaac 1297
Oy 1680 ctgacaacatttcgagcggcagcacttaacgcatatttaactgatgtctatgaaggaatcga 1739
Db 1298 acttaagaggaattgaaatccaggttctgcaacgctagctcgaagctatcagaagcgag 1357
Oy 1740 gttcttgaatttctgcatgcttgaacacacttgcatacagaagaatggaacttgaagag 1799
Db 1358 gtccacaacattgattgattgtctgtatgtagatggaatgtaacattgatactacttga 1417
Oy 1800 ttctgtgcgcagcagcagtcagtccttaacgcttga 1834
Db 1418 ttattactgtcactatgcataggaacaaagcttga 1452

RESULT 14
AAC48741
ID AAC48741 standard: DNA; 1392 BP.
XX
AC AAC48741;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 58595.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KM Protein identification; signal transduction pathway;
KM Metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.

XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
XX
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
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Best Local Similarity	51.5%;	Pred. No. 7.5e-36;		
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Db      568  gaattctggagctctgtgcatatgtatattctcttgaagtggttcccgcatctgg 627
Oy      1326  gcacgaacgaatcagaatattcgcattctgtgttgagaagctatcccaacttgat 1385
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Oy      1506  caaagc-----agatcccgctgacatattcattcagatttaagaacatacctc 1559
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Oy      1920  ttgacacaggaatca 1934
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RESULT 15
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XX
XX      AAV36878;
AC
XX
XX      12-OCT-1998 (first entry)
DT
XX
XX      Nucleotide sequence of ATCDPK1A PK domain.
DE
XX
XX      ATCDPK1A; protein kinase; PK; tolerance; drought; salinity; cold; heat;
KW      fruit; ornamental; vegetable; cereal; field crops; ds.
XX
XX      Aradopsis sp.
OS
XX
XX      Key      Location/Qualifiers
XX      CDS      97..918
XX      FT      /tag=
XX      FT      /product= "ATCDPK1A PK protein"
XX      FT      /note= "no stop codon specified"

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PN      W09826045-A1.
XX
XX      18-JUN-1998.
PD
XX
XX      12-DEC-1997; 97MO-US23019.
PF
XX
XX      13-DEC-1996; 96US-0032966.
PR
XX
XX      (GEHO ) GEN HOSPITAL CORP.
PA
XX
XX      Sheen J;
PI
XX
XX      WPI; 1998-348509/30.
DR
XX
XX      P-PSDB; AAW49837.
PT
XX
XX      Protecting plants against environmental stress - by introducing
XX      protein kinase domain-containing gene; calcium dependent protein
XX      kinase gene or calcium/calmodulin-dependent gene
XX
XX      Claim 17; Fig 5; 62pp; English.
XX
XX      This is the nucleotide sequence of the ATCDPK1A protein kinase (PK)
XX      domain isolated from the Aradopsis cDNA library, and used in the method
XX      of the invention to protect plants against environmental stress. The
XX      methods can be used for improving the tolerance of plants to
XX      environmental stresses such as drought, salinity, cold and heat. They
XX      provide for increased production efficiency, as well as for improvements
XX      in quality and the yield of crop plants and ornamentals. The methods
XX      contribute to the production of high quality and high yield agricultural
XX      products, e.g. fruits, ornamentals, vegetables, cereals, and field crops.
XX
XX      Sequence 1020 BP; 265 A; 194 C; 280 G; 277 T; 4 other:
XX

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Query Match      9 3%; Score 219.8; DB 19; Length 1020;
Best Local Similarity 57.4%; Pred. No. 1e-35;
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Job time: 6540 sec

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Db	361	gfnstlaagtlccvgatlcvgacvgacvgcgvggacacaaacvgccvgvggtvggcvtvgccvgcc	420
Qy	421	cgtaeccggtccvgvgvgcgvgagcccggtccvgccvgvggtvgtcvgccgtccvgccvgaggt	480
Db	421	cgtaeccggtccvgvgvgcgvgagcccggtccvgccvgvggtvgtcvgccgtccvgccvgaggt	480
Qy	481	cgagcccgagvggtctcttcaagcvgccggttcccgcccgcccgcccgcccgcccgagacataa	540
Db	481	cgagcccgagvggtctcttcaagcvgccggttcccgcccgcccgcccgcccgcccgagacataa	540
Qy	541	agacccagcccgcccgagagvgctgvggtvgvgvgvgagcccaagagvggatactccvgagvg	600
Db	541	agacccagcccgcccgagagvgctgvggtvgvgvgvgagcccaagagvggatactcccgagvg	600
Qy	601	agvgagvgcvtvgvgcvgctcvtgvcvgccvgcvtvgvgagvgcccgvgatvgvgvgcgvgagag	660
Db	601	agvgagvgcvtvgvgcvgctcvtgvcvgccvgcvtvgvgagvgcccgvgatvgvgvgcgvgagag	660
Qy	661	gvgcatctvggacaaagvgcgttcvgvggtctctcgaaagaaactcvgccvgagtaagctcvggag	720
Db	661	gvgcatctvggacaaagvgcgttcvgvggtctctcgaaagaaactcvgccvgagtaagctcvggag	720
Qy	721	agvgagvgcvtvgvgvgvgggccacatctcvggacaaactctcgcgcgtcvgtaaaagvggagat	780
Db	721	agvgagvgcvtvgvgvgvgggccacatctcvggacaaactctcgcgcgtcvgtaaaagvggagat	780
Qy	781	acaaagvgagagacvgctcvgcgttcaagatcatcgcgcaaaagtaagatgacaaacvgacatat	840
Db	781	acaaagvgagagacvgctcvgcgttcaagatcatcgcgcaaaagtaagatgacaaacvgacatat	840
Qy	841	ccatctvgagvgatctctgtatgaaagataaaattctggaagvggtatcatagvggcacataatc	900
Db	841	ccatctvgagvgatctctgtatgaaagataaaattctggaagvggtatcatcaagvggcacataatc	900
Qy	901	tcgtcaaatctcagtatactgcatgvtgagvgatvggcctcaatgctcaactctgcatvggagatat	960
Db	901	tcgtcaaatctcagtatactgcatgvtgagvgatvggcctcaatgctcaactctgcatvggagatat	960
Qy	961	gtcgagvgvggagaaatctgcataagacagatatctagccagvgcgvgvggatatcacagvggag	1020
Db	961	gtcgagvgvggagaaatctgcataagacagatatctagccagvgcgvgvggatatcacagvggag	1020
Qy	1021	atvgccaaagvgcagatctgtgtacagattcttgagcgttagtagccttcgtcactccctccagvgg	1080
Db	1021	atvgccaaagvgcagatctgtgtacagattcttgagcgttagtagccttcgtcactccctccagvgg	1080
Qy	1081	tavgtcacatcgatcttggaagccagagaaattccttctcaacccagvggatatgaatgctc	1140
Db	1081	tavgtcacatcgatcttggaagccagagaaattccttctcaacccagvggatatgaatgctc	1140
Qy	1141	ccatvgaaagtvgatgatttgcgtctcctgattctcatctagaccagagatgaagvgcttaatg	1200
Db	1141	ccatvgaaagtvgatgatttgcgtctcctgattctcatctagaccagagatgaagvgcttaatg	1200
Qy	1201	atattggtvggagvgcatatatatgtgcccccgagvggttttaacacagatcatatagtatvg	1260
Db	1201	atattggtvggagvgcatatatatgtgcccccgagvggttttaacacagatcatatagtatvg	1260
Qy	1261	aagcagacatctvgaggtataggtgttcataaacgttacatctgctctgtgtgacgtccggcat	1320
Db	1261	aagcagacatctvgaggtataggtgttcataaacgttacatctgctctgtgtgacgtccggcat	1320
Qy	1321	tcctvggacagaaacvgaaatccaagaaatatccgatctgvtgtvgagcvtgatacccaacttvg	1380
Db	1321	tcctvggacagaaacvgaaatccaagaaatatccgatctgvtgtltvgagcvtgatacccaacttvg	1380
Qy	1381	atgataccaacgttggccatacagataccgcgaaagccaaagattttgtgaagagattttcga	1440
Db	1381	atgataccaacgttggccatacagataccgcgaaagccaaagattttgtgaagagattttcga	1440
Qy	1441	acaaaggttcgcgcaaaagatgacgcggtctcaagacactgatactacttcgtgttgcgag	1500

Db 1441 acaaaagattaccgcaaaagaattgcgcgtgtcttaagaacagcagactacccctgtgtcgag 1500
 Oy 1501 atgacaaagcgagatccgcgtgtgacatactatcttcagatlaatlaagcaatactcc 1560
 Db 1501 atgacaaagcgagatccgcgtgtgacatactatcttcagatlaatlaagcaatactcc 1560
 Oy 1561 gcgcacaccccttaaacggtgtgtgacataaaggacataccaagccttaaggaaatg 1620
 Db 1561 gcgcacaccccttaaacggtgtgtgacataaaggacataccaagccttaaggaaatg 1620
 Oy 1621 aactttgtatctcaaacctcagtttaactgtgcgaacctagaagcttggtgtgacac 1680
 Db 1621 aactttgtatctcaaacctcagtttaactgtgcgaacctagaagcttggtgtgacac 1680
 Oy 1661 ttgacaacttcggaacggaactaaacggaatatlaactgatgtacatgaagaaatcgag 1740
 Db 1661 ttgacaacttcggaacggaactaaacggaatatlaactgatgtacatgaagaaatcgag 1740
 Oy 1741 ttcttgaaattttgcatgtgttggaaccccttgacacagaagaatgagccttgaagat 1800
 Db 1741 ttcttgaaattttgcatgtgttggaaccccttgacacagaagaatgagccttgaagat 1800
 Oy 1801 tctgtgcgcgaacaaatcagtccttaacagcttgaaggacacttggaaggtgagagatg 1860
 Db 1801 tctgtgcgcgaacaaatcagtccttaacagcttgaaggacacttggaaggtgagagatg 1860
 Oy 1861 ctggaaacagcttccaggaatttgaaacaaaggagcaaccgagatcatatcagttgaaga 1920
 Db 1861 ctggaaacagcttccaggaatttgaaacaaaggagcaaccgagatcatatcagttgaaga 1920
 Oy 1921 tagcacagggatlaaatctgtgcccacacatataccatctgttcaagaactgatacaga 1980
 Db 1921 tagcacagggatlaaatctgtgcccacacatataccatctgttcaagaactgatacaga 1980
 Oy 1981 aatccgattgcaagactaaactctctcgggttaccaaattttacatgtgtcaacaata 2040
 Db 1981 aatccgattgcaagactaaactctctcgggttaccaaattttacatgtgtgtcaacaata 2040
 Oy 2041 ggggcaccaataaagaacggcatltaaggcatttgaaaaaagaatgtatcttctctt 2100
 Db 2041 ggggcaccaataaagaacggcatltaaggcatttgaaaaaagaatgtatcttctctt 2100
 Oy 2101 ctaatttlaaagcgcctctttagaacccctatgcatgtttcccccgcgcctcatc 2160
 Db 2101 ctaatttlaaagcgcctctttagaacccctatgcatgtttcccccgcgcctcatc 2160
 Oy 2161 cccctgtgtaaatatgatcatctatctctgtgtcgtgcgtgcgcgtgtgtcatcaagt 2220
 Db 2161 cccctgtgtaaatatgatcatctatctctgtgtcgtgcgtgcgcgtgtgtcatcaagt 2220
 Oy 2221 ttcttttagagaatacatgtaaagatctcttttgtaagtgaatcgaaatgatatgtgttcaa 2280
 Db 2221 ttcttttagagaatacatgtaaagatctcttttgtaagtgaatcgaaatgatatgtgttcaa 2280
 Oy 2281 gaataatagtgcatgtgttcttcttttggccagtaaaaaaataaataatctc 2340
 Db 2281 gaataatagtgcatgtgttcttcttttggccagtaaaaaaataaataaataatctc 2340
 Oy 2341 gaggcggggcgttacacatccccccctgaagc 2374
 Db 2341 gaggcggggcgttacacatccccccctgaagc 2374
 RESULT 2
 ; Sequence 7, Application US/09347801
 ; Patent No. 6262345
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Steve
 ; APPLICANT: Lee, Jian Ming
 ; TITLE OF INVENTION: Plant Protein Kinases
 ; FILE REFERENCE: BB-1171

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CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO: 7
LENGTH: 498
TYPE: DNA
ORGANISM: Trifolium aestivum
FEATURE:
NAME/KEY: unsure
LOCATION: (498)
US-09-347-801-7

Query Match
Best Local Similarity 67.3%; Pred. No. 2e-34; Length 498;
Matches 332; Conservative 0; Mismatches 155; Indels 6; Gaps 4;

QY 972 gaattcgtacagaattatgaagcagagcgagagatcacagaggaagatgccaaagcg 1031
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 gaactactgtataagaatattgagagaggtggaagatattctgaagaagatgcaaggtc 61

QY 1032 atgtgtacagattttgagcgtagtagcctctgtcatcttcagggggtagtgacgt 1091
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 gtatctgtcaaatatttgtagtgatcatcttgcacatctcaaggtgtgtctacg 121

QY 1092 gatttgaagcagagaattcttccttcacaacagagatgaagaatgtctccatgaagttg 1151
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 gatctgaacacagagaattcttcacatctcagaaagagaacaccccttgaaggtc 181

QY 1152 atgtattgtctcctcattcatctagacacagatgaagcgcttaagtattgttga 1211
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 atagacttggctgtgctgacttctgaagccagatgaagagctcaacgacattgttga 241

QY 1212 agtgcattatgttgc-cccagaggtttacacagatcatatagatggaagcagacat 1270
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 agtgcattatgttgcctcccgaggtgtctcatcgtactatgacgagaggtat 301

QY 1271 -ttgagtagtgcataacgtatattctgtctgtgcaatggccattc--tgggc 1327
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 gtggagcattggaatattgctcatattgtcttgttggagacgacttctctgggc 361

QY 1328 accaagatcagagatatctcgatctgtgtgagagcgctaccacacttgatgttc 1387
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 accaagatcagagatatctccagcttcccttaagcaaaacacatttgaagc 421

QY 1388 accgtgctacagtaacagctgaagcgaagattttgtgaagagatttctgaacaaga 1447
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 cccaagcctactcctctcgcggaaccaag--actgttaaaagggtctataaga 479

QY 1448 ttacgcgaaga 1460
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Db 480 ttaccaagaga 492

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RESULT 3
US-08-464-164-1

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Sequence 1, Application US/08464164
Patent No. 5614195
GENERAL INFORMATION:
APPLICANT: Tomley, Fiona M.
APPLICANT: Dunn, Paul P. J.
APPLICANT: Bumstead, Janene M.
APPLICANT: Vermeulen, Arno N.
TITLE OF INVENTION: Coccidiosis poultry vaccine
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: Akzo No. 5614195el Patent Department
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland

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COUNTRY: U.S.A.
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,164
FILING DATE: June 2, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: C-terminal
ORIGINAL SOURCE:
ORGANISM: Elmeria maxima
STRAIN: Houghton
DEVELOPMENTAL STAGE: sporozoite
IMMEDIATE SOURCE:
LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
CLONE: Em70-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1368
US-08-464-164-1

Query Match
Best Local Similarity 6.4%; Score 153; DB 1; Length 1400;
Matches 386; Conservative 0; Mismatches 345; Indels 6; Gaps 2;

QY 759 ggcgtcgtcaagaagggcggtacaaagcgcgtgcgtcaagatcatcccaaa 818
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 25 GTCATCTTATGCAAGACGACAGATTAACGACACAGAAATATGCAATTAATCTTAA 84.

QY 819 gctaaatgcaacgcaatattccattgagatgtctgtagaagaataaatttga 878
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 85 CGTCAACTAAACAGAACAGATTAAGAAATTTATTTAAAGAAATTAATTTA 141

QY 879 gcgttatcagggcacaatattctgtcaaatctatgatgatgttgagagcctcaat 938
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 142 AAGAAATTAATGATCTCTAATATCATGAAATTAATTAATTTGAGGATTAAGATAC 201

QY 939 gtctacattgcatggaattaatggaaggaaggaatgtctagaacaataltaacaga 998
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 202 TTTTATCTTGTGTACAGATATATACAGAGAGAAATTTATTTGATGAATTTATTAACGA 261

QY 999 ggcggagatacacagaggaagatgccaagcgatgtgtlacagatttgaacgtatga 1058
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 262 AAA--AGATTCAACGAGGCGGATGACGCTGTAGTACGTCAGGTCTATCGGGTATA 318

QY 1059 gccctcgtcatcttcagggggtgtagtcatgtgatttgaagcagaagaattcttctc 1118
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 319 AATTATATGATGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 378

QY 1119 acaaccagagatgaagaatgtcccatgaagtgtatgtatttggctctcatcatt 1178
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 GAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 438

QY 1179 agaccagatgaagcgttaatgatattgttgaagtcataatttgttccccaaggtc 1238
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Db 439 GAGCCCCAAAAAATGAGATATAATTCGGAGCCGGCTACTACATTGCCCTGAGGTG 498
Qy 1239 ttacacagatcatatagatgtaagacagacatttgagatagatgtaacgtaac 1298
Db 499 CTGCACGGACATACGATGAGAGAAATGCGACGCTGGCTACGCGGTATCTCTATATC 558
Qy 1299 ctgctcttgagcagtcgagcattctcgtgcaacagacatcagagatattccgactctg 1358
Db 559 CTCTCTCTGTGGTTGTCCTCATTTTACGAGCAAAATGAAATTTCTAAAGAAATGC 618
Qy 1359 ttgagagctgattcccaacttgatgattcaccgttgacctagatcagctgaagctaa 1418
Db 619 GAGAAAGGAAATTCACCTTCGATTTACACAGTGGCGCTAAGGTAGCGACGACGAAAA 678
Qy 1419 gattttggaagagattctcgaacaaagattacccgcaaaagatgaccgctgttcaagca 1478
Db 679 GATTTAATTAGGAAGATGTTAGCATATGTACCTCAATGAGTATATACGAAAAAGATGCA 738
Qy 1479 ctgaactcacttggt 1495
Db 739 TTAGATCATCATGAT 755

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RESULT 4

US-08-338-057-1

Sequence 1, Application US/08338057

Patent No. 5795741

GENERAL INFORMATION:

APPLICANT: Tomley, Fiona M.

APPLICANT: Dunn, Paul P. J.

APPLICANT: Bumstead, Janene M.

APPLICANT: Vermeulen, Arno N.

TITLE OF INVENTION: Coccioidosis poultry vaccine

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Organon Teknika Corporation

STREET: 1330 Pilecard Drive

CITY: Rockville

STATE: Maryland

COUNTRY: U.S.A.

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/338,057

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 93.30907.9

FILING DATE: 12-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Gormley, Mary E.

REGISTRATION NUMBER: 34,409

TELEPHONE: (301) 258-5200

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1400 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: C-terminal

ORIGINAL SOURCE:

ORGANISM: Elmeria maxima

STRAIN: Houghton

DEVELOPMENTAL STAGE: sporozoite

IMMEDIATE SOURCE:

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LIBRARY: sporozoite cDNA cloned in Lambda ZAP11
CLONE: Em/0-1
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1368
US-08-338-057-1

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Query Match 6.4%; Score 153; DB 1; Length 1400;
Best Local Similarity 52.4%; Pred. No. 2.8e-25;
Matches 386; Conservative 0; Mismatches 345; Indels 6; Gaps 2;

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Qy 759 gcgcgtgcaagaaggcgagttacaaaggacagaccgctgcgcaagatcgcacaa 818
Db 25 GTCATCTTATGCAAGAGCAAGATTAACAGCACAGAAATATGCAAGAAAGTAAATATCA 84
Qy 819 gctaaagtgaacaggaatatacattgagagattcgtgtagaagaataatttga 878
Db 85 CGTCAAGTAAACAGAAAGACGATTAAGAAATTAATTAAGAAAGTTGAATTAATTT--A 141
Qy 879 gcgtatcagggcacaaatactcgtcaattctcatgatgcatgtgagagtgcccaat 938
Db 142 AAGAAATTAAGATCATCTCTAATATCATGAATTAATTAATTTCTTGAGATTAAGATAC 201
Qy 939 gtctacattgcatggaattatgtgagggaggaattctgtagaagaataattagccaga 998
Db 202 TTTTATCTTGTTCACAGATATATACAGAGAGGAGAAATTAATTAATTAATTAATCA 261
Qy 999 ggcggagatcacacagagagagatgccaaagcgtctgttagaagatttgagcgtgta 1058
Db 262 AAA---AGATTACAGCGAGCGGATGCGATCGATAGCTAGCTAGGTTCTATCGGGTATA 318
Qy 1059 gcctctgcatcctcgaaggagtagtgcgtgatttgagccagagaattcccttcc 1118
Db 319 AATTATATGATCGATTAATAAATAGTTCATAGAGATTAAGACAGAAATTAATTAATTA 378
Qy 1119 acaaccagggatgaaatgctcccaagaagtgtgattgatttgctctctgattccat 1178
Db 379 GAGAAATTAATAAATAAGATGCAAAATATACGAATTAATTAATTAATTAATTAATTA 438
Qy 1179 agaccagatgaaggcttcaatgtatgttgagagtcgcatatctgtccccaagaggt 1238
Db 439 GAGCCCCAAAAAATAATGAAAGATTAATAATGCGGCGGATACATTAATGCCCCCTGAGGTG 498
Qy 1239 ttacacagatcatatagatgtaagacagacatttgagatagatgtaacgtaac 1298
Db 499 CTGCACGGACATACGATGAGAGAAATGCGACGCTGGCTACGCGGTATCTCTATATC 558
Qy 1299 ctgctcttgagcagtcgagcattctcgtgcaacagacatcagagatattccgactctg 1358
Db 559 CTCTCTCTGTGGTTGTCCTCATTTTACGAGCAAAATGAAATTTCTAAAGAAATGC 618
Qy 1359 ttgagagctgattcccaacttgatgattcaccgttgacctagatcagctgaagctaa 1418
Db 619 GAGAAAGGAAATTCACCTTCGATTTACACAGTGGCGCTAAGGTAGCGACGACGAAAA 678
Qy 1419 gattttggaagagattctcgaacaaagattacccgcaaaagatgaccgctgttcaagca 1478
Db 679 GATTTAATTAGGAAGATGTTAGCATATGTACCTCAATGAGTATATACGAAAAAGATGCA 738
Qy 1479 ctgaactcacttggt 1495
Db 739 TTAGATCATCATGAT 755

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RESULT 5

US-08-668-416-1

Sequence 1, Application US/08668416

Patent No. 5843722

GENERAL INFORMATION:

APPLICANT: Tomley, Fiona M.

APPLICANT: Dunn, Paul P. J.

APPLICANT: Bumstead, Janene M.

CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."
US-07-951-715A-20

Query Match 6.4%; Score 151.6; DB 1; Length 1349;
Best Local Similarity 53.9%; Pred. No. 5,6e-25;
Matches 335; Conservative 0; Mismatches 284; Indels 3; Gaps 1;
QY 883 tatcaggacacataatctcgtcaaatctatgatgcatgtgagtgccatcgtct 942
DB 19 TCTCGGCCAGCCCAACGCTGTGGCTCCGCCCGCTACGAGGACAGACAGCGCTGC 78
QY 943 acattgtcatgaaatattgtgagagagaaattgtctagacagaaatattagccaagagcg 1002
DB 79 ACCGTGTCATGAGCTGTGCGGGGGAGCTTTCAGCCGATCATTCGCCGGGGCC 138
QY 1003 ggaatataccagagaaagtgtccaaagagatgtgttgaagattttgaagcgtttagcct 1062
DB 139 AG---TACACGAGAGCGCGCGCGCGAGCTGCTGCCCATCGTCAGATGTGCACA 195
QY 1063 tctgtcatcttcaggaggtgagtcgtgcatcgtgatttgaagcagagaaatttcctttacaa 1122
DB 196 CTTGCCACATCCATGGGGGTGATGACACCGGACATCAAGCCCGAGACTTCTCTCTCA 255
QY 1123 ccaggagatgaataatgtcccatgaagtgtgatttggctctctgatttcattatagac 1182
DB 256 GCAAGGACGAGACCGCGCTCAAGGACACGACTTTCGGCTCTCCGCTTCTTCAGG 315
QY 1183 cagatgaagaagcttaatgattgttggaaagtgcataatattgttgcacagaggttttac 1242
DB 316 AGGGGAGCTGTCAAGGACATCTCGGACAGGCTACTACATCAATCGGCCCGAGGTCTCA 375
QY 1243 acaagatcatatagttgagacagacatttggagttagttgataaagttacattctgc 1302
DB 376 AAGAGAAAGTACGGCCGAGGCGGACATCTGGAGCTCGGCTCATGCTTACATCTTTC 435
QY 1303 tctgtgcagtcgagcattcttggagcagacagaaatcagaaatattcagatctgtgtga 1362
DB 436 TCGCGGGCTGCTCCCTTCTGGGCGAGAGAGAGAGCATCTTCCACGGCGATCTCG 495
QY 1363 gagctgattcccaacttgaattcaacgctggcctaacagatcagctgaagtaagatt 1422
DB 496 GAGGGCAGCTTCACTCTCCACGCGACCATGCGCACACATCTCGCGGAGCAAGATC 555
QY 1423 ttgtgaagaagatttgaacaaagattaccgaaagaatgacgctgttcaagacctga 1482
DB 556 TCGTAAAGAGAGTGTCTCAACATCAACCCCAAGAGCGGCTTCCAGGCTTCAAGTCTCA 615
QY 1483 ctcatccttgtgtcgagatga 1504

Db 616 ATCACCCATGATCAAGAGAGA 637
RESULT 7
US-08-459-448A-20
Sequence 20, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Kozielec, Michael G.
APPLICANT: Desai, Nalin M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Kyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlino, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIVA
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
OTHER INFORMATION: disclosed in Figure 30."
US-08-459-448A-20

Query Match 6.4%; Score 151.6; DB 2; Length 1349;
 Best Local Similarity 53.9%; Pred. No. 5.6e-25;
 Matches 335; Conservative 0; Mismatches 284; Indels 3; Gaps 1;

QY 883 taccaggaacaaataatcgtcaaatctatagatgcatgtagatggcctcaatgctc 942
 Db 19 TCTCCGGCAGCCCAACGTGTGGGCTCCGGCGGCGGTACAGAGCAAGAGAGTGC 78
 QY 943 acattgcatgaattatgtgagggagagaattcttagacaagaattatagccagagcg 1002
 Db 79 ACCCTGTATGAGAGTGTGCGGGGGGGAGACTCTTCCAGCCGATCATCGCCGGGCGC 138
 QY 1003 ggaatatacaagaagaatgccaagaagcattgtgtacagattttgagcgttagacct 1062
 Db 139 AG---TACACGAGAGCGCGCGCGCGGAGCTCTGCGCCCATCGTGCAGATCGTGCACA 195
 QY 1063 tctgtcattctcaaggaggttagtgcacgtgatttgaagccaagaattccttccacaa 1122
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 QY 1123 ccaggatgaagaatgtcccaagaattgattgatttggctctcctgattcattagac 1182
 Db 256 GCAAGAGCAGAGAGCGCGCGCTCAAGGCCACCGACTTCGGCTTCCTTCCTCAAGG 315
 QY 1183 cagatgaaggcttaatatgttgaagtgcattatgttgcacagaaggtttac 1242
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 Db 376 AGAGGAATACGCGCCCGGAGCGCGACATCTGGAGCGTCCGCTCATGCTCTACATCTTC 435
 QY 1303 tctgtgagcagtcggcattcttgagcagaacagaatcagaatattcgaattgtgtga 1362
 Db 436 TCGCGGCGTGTGCTCTCTTGTGGGAGAGAGAACGGCATCTTCCACCGCATCTTC 495
 QY 1363 gacctgatacccaatttgaatgattacccgtggcctacagtagtcaagcagaatt 1422
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 QY 1423 ttgtgaagagatttctgaacaaagatttacgcaaaagaatgaacgctgttcaagcactga 1482
 Db 556 TCGTGAAGAAGATGCTCAACATCAACCCCAAGAGGCGCTCAAGGCTCTCAAGTCTCA 615
 QY 1483 ctcatccttggttcgagatga 1504
 Db 616 ATCACCACATGATCAAGAAGA 637

RESULT 8

US-08-459-595A-20
 ; Sequence 20, Application US/08459595A

; Patent No. 6018104

; GENERAL INFORMATION:

; APPLICANT: Kozziel, Michael G.

; APPLICANT: Desai, Nalini M.

; APPLICANT: Lewis, Kelly S.

; APPLICANT: Kramer, Vance C.

; APPLICANT: Warren, Gregory W.

; APPLICANT: Ewola, Stephen V.

; APPLICANT: Crossland, Lyle D.

; APPLICANT: Wright, Martha S.

; APPLICANT: Meriott, Ellis J.

; APPLICANT: Launis, Karen L.

; APPLICANT: Rothstein, Steven J.

; APPLICANT: Bowman, Cindy G.

; APPLICANT: Dawson, John L.

; APPLICANT: Dunder, Erik M.

; APPLICANT: Pace, Gary M.

; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6018104artis Corporation
 STREET: Patent & Trademark Dept., 520 White Plains
 STREET: Rd., POB 2005
 CITY: Tarrytown
 STATE: New York
 COUNTRY: USA
 ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,595A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIY3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8582

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

OTHER INFORMATION: /note="cDNA sequence for maize

OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as

OTHER INFORMATION: disclosed in Figure 30."

US-08-459-595A-20

Query Match 6.4%; Score 151.6; DB 3; Length 1349;
 Best Local Similarity 53.9%; Pred. No. 5.6e-25;
 Matches 335; Conservative 0; Mismatches 284; Indels 3; Gaps 1;

QY 883 taccaggaacaaataatcgtcaaatctatagatgcatgtagatggcctcaatgctc 942
 Db 19 TCTCCGGCAGCCCAACGTGTGGGCTCCGGCGGCGGTACAGAGCAAGAGAGTGC 78
 QY 943 acattgcatgaattatgtgagggagagaattcttagacaagaattatagccagagcg 1002
 Db 79 ACCCTGTATGAGAGTGTGCGGGGGGGAGACTCTTCCAGCCGATCATCGCCGGGCGC 138
 QY 1003 ggaatatacaagaagaatgccaagaagcattgtgtacagattttgagcgttagacct 1062
 Db 139 AG---TACACGAGAGCGCGCGCGGAGCTCTGCGCCCATCGTGCAGATCGTGCACA 195
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 QY 1123 ccaggatgaagaatgtcccaagaattgattgatttggctctcctgattcattagac 1182
 Db 256 GCAAGAGCAGAGAGCGCGCGCTCAAGGCCACCGACTTCGGCTTCCTTCCTCAAGG 315

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Db	316	AGGGGAGACCTCTAAGGAGACATCGTGGCAGCGCCCTACTACATCGGCCCGAGGTGTCA	375
OY	1243	acagatcatatagtatggaagcagacaatttgtagtataagtggtcataaagttacatctgc	1302
Db	376	AGAGAGAGTACGGCCCGGAGCGCGACATCTGGAGGCTCCGGCTCAATGCTCATCTATCTCC	435
OY	1303	ctcttggcagtcgcgcacatcttggaacgaacagaaatcaggaattatccgattctgtgtga	1362
Db	436	TCCGCGGGCGTCCCTCTTGGGCGAGAGACGAGAACGGCATCTTCACCGCATCTCTGC	495
OY	1363	gagcttgatcccaactttgatgatcttcaacgcgtgtgcctaacgatatcagctgaagctaaagat	1422
Db	496	GAGGGCAGCTTGGACCTCTCCAGCGAAGCCATAGGCCACATCTTCGCGGGAGGCAAGGATTC	555
OY	1423	ttgtgtaagagattcttgaacaaagattaccgcaaaagaaatgaacgcgtgttcaagaactga	1482
Db	556	TCTGTCAGAGAGATGCTCAACATCAACCAACCCCAAGAGGGGCTCACGGCGTTCCAGAGTCTCA	615
OY	1483	ctcatccttggtgtgcgagatga	1504
Db	616	ATCACCCATGATCAAGAAGA	637

RESULT 9
 US-08-459-504B-20
 : Sequence 20, Application US/08459504B
 Patent No. 6075185
 : GENERAL INFORMATION:
 APPLICANT: Kosziel, Michael G.
 APPLICANT: Desai, Nallni M.
 APPLICANT: Lewis, Kelly S.
 APPLICANT: Kramer, Vance C.
 APPLICANT: Warren, Gregory W.
 APPLICANT: Evola, Stephen V.
 APPLICANT: Crossland, Lyle D.
 APPLICANT: Wright, Martha S.
 APPLICANT: Merlin, Ellis J.
 APPLICANT: Launis, Karen L.
 APPLICANT: Rothstein, Steven J.
 APPLICANT: Bowman, Cindy G.
 APPLICANT: Dawson, John L.
 APPLICANT: Dunder, Erik M.
 APPLICANT: Pace, Gary M.
 APPLICANT: Suttle, Janet L.
 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 NUMBER OF SEQUENCES: 94
 INSECTICIDAL ACTIVITY IN MAIZE
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: No. 6075185artis Corporation
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park
 STATE: NC
 COUNTRY: USA
 ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,504B
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/459,595
 FILING DATE: 02-JUN-1995
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 25-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991

```

1  ATTORNEY/AGENT INFORMATION:
2  NAME: Meigs, J. Timothy
3  REGISTRATION NUMBER: 38,241
4  REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
5  TELECOMMUNICATION INFORMATION:
6  TELEPHONE: (919)541-8587
7  TELEFAX: (919)541-8689
8  INFORMATION FOR SEQ ID NO: 20:
9  SEQUENCE CHARACTERISTICS:
10     LENGTH: 1349 base pairs
11     TYPE: nucleic acid
12     STRANDEDNESS: single
13     TOPOLOGY: linear
14     MOLECULE TYPE: cDNA
15     HYPOTHETICAL: NO
16     FEATURE:
17         NAME/KEY: CDS
18         LOCATION: 3..1226
19         OTHER INFORMATION:
20             OTHER INFORMATION:
21                 /note="cDNA sequence for maize
22                 pollen-specific calcium dependent protein kinase gene as
23                 disclosed in Figure 30."
24
25 US-08-459-504B-20

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Query Match	6.4%	Score 151.6	DB 3	Length 1349
Best Local Similarity	53.9%	Pred. No. 5.6e-25		
Matches 335	Conservative 0	Mismatches 284	Indels 3	Gaps 1
QY 883	latacaggcacaaataatctcgtlcaaatattcatatgatcagctgtgaagatgagcctcaatgtct	942		
Db 19	TCTCCGGCCACCCCAACCTGTGGGCTCTCCGGGCGCGNACGAGACAAGACAGCTGC	78		
QY 943	acatgtgaatgaatatagtgtagggaggaagaaattgcttagacgaatatatagccaaagcgc	1002		
Db 79	ACCTCGTATGAGCTGTGCGCGGGGGAGACTTTTGACACCGATCAATGCGCGGGGCG	138		
QY 1003	ggagatacacagagagaaatgtccaaagsgaatgttgtatcagaatttgagcgttagagcct	1062		
Db 139	AG---TACACGAGCGCGCGCGCGGAGCGTGCCTGGCGCATCGTCGACATCGTGACNA	195		
QY 1063	tcctgtacattccaggggttagtgcatcgttgatttgaagccagaaatctcctttcaaaa	1122		
Db 196	CTCTCCACCTCCATGGGGGTATGCACCGGACATCAACCCGAGAACTTTCGTGCTCA	255		
QY 1123	ccagaggatgaanaatcgtcccatgaagtgtgaattgtattgtctctgtattcatatagac	1182		
Db 256	GCAAGAGCAGAGAGCGCGCGCTCAAGGCAACGAACTTGGGCTCTCCGCTTTCTCAAG	315		
QY 1183	cagatgaagaaggcttaatgatattgttggaaatgcataattatgttgcgccagaagtttac	1242		
Db 316	AGGGCGAGCTCCTAGGAGACATCGTCGGCACCGCTTACATATGGCCGCCAGAGGTCA	375		
QY 1243	acaatcatatagatcatgtgaagcagacaatttggatlatagtgctcaataacgtaattctgc	1302		
Db 376	AGAGGAGTACGCGCCCGGAGCGCCACATCTTGAGCGCTCGGCTCATGCTTACATCTTCC	435		
QY 1303	tcctgtgcagtcgycatcttcgycacgaaacagaataatcagaataatccgactgtgtga	1362		
Db 436	TTCGCGGCGCTGCCTCTTCTTGCGCAGAGAACGAAACGGCATCTTCAACCCCATCTGC	495		
QY 1363	gaagctgtaccaaatttggatgatcatcacgctgagctacagtaatacgtgaagctaaagatt	1422		
Db 496	GAGGGCAGCTTGACCTCTCCAGCGAGCGCAATGGCCACATCTGCCGGGAGCAAGGATC	555		
QY 1423	ttgtgaagaatattcttgaacaaagatatacgcnaaagaatgacgcgttctcaacgta	1482		
Db 556	TTCGTCAGAGAGATGCTCAACATCAACCCCAAGAGGCGGCTCAGCGCTTCCAGGTCTCA	615		
QY 1483	ctatcctctgttgcgaagatga 1504			
Db 616	ATACACCATGATCAATCAAGAGA 637			

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RESULT 10
US-08-459-444-20
: Sequence 0, Application US/08459444A
: Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Laundis, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: /note= "cDNA sequence for maize
pollen-specific calcium dependent protein kinase gene as
disclosed in figure 30."
SEQUENCE CHARACTERISTICS:
LENGTH: 1349 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1226
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-08-459-444-20

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Query	Match	Similarity	6.4%	Score	151.6	DB	3	Length	1349
	Local	Similarity	53.9%	Prod	N5.6e-25				
	Matches	335	Conservative	0	Mismatches	284	Indels	3	Gaps
QY	883	tatcagggcacataatctcgtcaaatlctatgatgatcgttgaagatggcctcaatgltct	942						
Db	19	TCTCCGGCCAGCCCAAGCGTGTGGGCGTCCGGGGCCGTCACGACGACGACGACGCGTGG	78						
QY	943	acatcgtcatggaattatgttgaagggaagaaattgctatagacagaataattagccagaagcg	1002						

Db	79	ACCTGTCATGAGACGTGTGGCGGGGGGAGACTTTCACCGCATATCGGCCGGGGACC	138
QY	1003	ggagatcacagagaggaatgaccaaagcgatggtgtacagaattttagagctagacct	1062
Db	139	AG--TTACAGGAGACGGGGCGCCGAGACTGTGGCGCCATCGTGAGATCGTGACA	195
QY	1063	tctctacattcagggggtgtgtacgcgfatgtttagagccaaagaatttcctttccaa	1122
Db	196	CTCTCCACTCCATGGGGGTATGCACCGGAGACATCAAGCCGAGAACTTCGTGCTCA	255
QY	1123	ccaggatgaaatgtcccatbaagttgatgatttgtctctgatttcaatgac	1182
Db	256	GCAAGGACGAGAGACGCCGCCCTCAAGGCCACCGACTTCGGCCTTCGCTTTCTTCAAG	315
QY	1183	cagatgaagagcttaatgatalgttgttgaagtgcataltatgtgtgcccaaggtttac	1242
Db	316	AGGCGAGCTGCTCAGGAGACATGTCGGCAGGCCCTACTACATCGCGCCGAGGTGCTCA	375
QY	1243	acagatcatatagatgaaagcagaacatttggatgataagtcatcaacgfatatctgc	1302
Db	376	AGAGGAAGTACGGCCCCGAGCGCCGACATCTGGAGCCTCGGCTCATGCTTACATCTTCC	435
QY	1303	tctgttcagtcgagccatttctggcagcgaacagaatcagaatatttcgcattcgtgttca	1362
Db	436	TCCGCGCGGTGCTCCCTTTGTGGGAGAGACGACGACGCGCATCTTACCGCCATCTGTC	495
QY	1363	gagctgtatcccaacttgaatctacgattcacgcgtgtgctacgatalcagctgaagctaaagt	1422
Db	496	GAGGGCAGCTTGAGCTCTCCAGGAGACCATGGCCACACATCTGGCGGAGGCAAGATTC	555
QY	1423	tctgtgaagagatttctgaaacaaagattaccgcgaagaatgacgcgtgttcaagcatca	1482
Db	556	TCTGTCAGAGAAATGCTCAACATCAACCCCAAGAGAGGGCTCAGCGGTTCAGTCTCA	615
QY	1483	ctcatccttggttgcgagatga	1504
Db	616	ATCACCATGATCTCAAGAAGA	637

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RESULT: 11
US-93-347-801-5
Sequence 5, Application US/09347801
Patent No. 6262345
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: Bb-1171
CURRENT APPLICATION NUMBER: US/09/347, 801D
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 5
LENGTH: 568
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (11)
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NAME/KEY: unsure
LOCATION: (148)

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? NAME/KEY: unsure
? LOCATION: (196)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (272)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (557)
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? LOCATION: (568)
US-09-347-801-5

Query Match 6.3%; Score 150.6; DB 4; Length 568;
Best Local Similarity 59.6%; Pred. No. 6.4e-25;
Matches 329; Conservative 0; Mismatches 176; Indels 47; Gaps 3;

QY 465 ccgtccgagcaggtcgaagcccaagaggtcttcaagcgccgtcccgccgctcg 524
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Db 55 cccatgagcagctcantcaacaccttcngatcttcaagcncctctccctccgctct 114

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Db 196 -----naggtgagctcgccctcgaaagacgttcgcttctgaagcagtttcggt 249

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QY 765 gtaagaaagggcgagtaagagggagacagccgctcgccgtcaagatccgcaagctaa 824
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Db 310 ggaagaaagggcgagtaagagggagacagccgctcgccgtcaagatccgcaagctaa 369

QY 825 atgacacagcaatccatcttgagagtggttcgtagagagtaaaatttgagagcgta 884
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Db 370 atgacacagcaatcttgctatagaggttgtaagagagagtgagagatctgaagggctta 429

QY 885 tcaaggacaaatctcgtcaaatctctatgacatgtagatgagatgacctcaatgctac 944
    |||||
Db 430 acagagacataagatctggtgcaattctatgaagcctatgaagatgatgac-atgttat 488

QY 945 atgtcatggaattatgtgagagagagagatgcttagaagaatataccaagagcgag 1004
    |||||
Db 489 atagct-ttgagatctgtgcaagagagagagatctgtagatagattcttcggggtgaa 547

QY 1005 agatacacagag 1016
    |||||
Db 548 agtacctcgag 559

RESULT 12
US-08-459-448A-26
; Sequence 26, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: KOZIEL, Michael G.
; APPLICANT: DESAI, Nalini M.
; APPLICANT: LEWIS, Kelly S.
; APPLICANT: KRAMER, Vance C.
; APPLICANT: WARREN, Gregory W.
```

```

?
? APPLICANT: Evola, Stephen V.
? APPLICANT: Crossland, Lyle D.
? APPLICANT: Wright, Martha S.
? APPLICANT: Merlin, Ellis J.
? APPLICANT: Launis, Karen L.
? APPLICANT: Rothstein, Steven J.
? APPLICANT: Bowman, Cindy G.
? APPLICANT: Dawson, John L.
? APPLICANT: Dunder, Erik M.
? APPLICANT: Pace, Gary M.
? APPLICANT: Suttie, Janet L.
? TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
? NUMBER OF SEQUENCES: 94
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: No. 5859336artis Corporation
? STREET: Patent & Trademark Dept., 520 White Plains
? STREET: Rd., POB 2005
? CITY: Tarrytown
? STATE: New York
? COUNTRY: USA
? ZIP: 10591-9005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: floppy disk
? OPERATING SYSTEM: IBM PC compatible
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/459,448A
? FILING DATE: 02-JUN-1995
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/951,715
? FILING DATE: 25-SEP-1992
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/772,027
? FILING DATE: 04-OCT-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Pace, Gary M.
? REGISTRATION NUMBER: 40403
? REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (919)541-8582
? TELEFAX: (919)541-8689
? INFORMATION FOR SEQ ID NO: 26:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 4162 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 1418..1427
? OTHER INFORMATION: /note= "start of mRNA"
? FEATURE:
? NAME/KEY: exon
? LOCATION: 1481..2366
? FEATURE:
? NAME/KEY: intron
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? NAME/KEY: exon
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? NAME/KEY: exon
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? FEATURE:
? NAME/KEY: intron
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OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
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LOCATION: 3499..3713
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NAME/KEY: exon
LOCATION: 3714..3811
FEATURE:
NAME/KEY: Promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-595A-26

Query Match 6.0%; Score 143; DB 3; Length 4162;
Best Local Similarity 53.6%; Pred. No. 7.6e-23;
Matches 349; Conservative 0; Mismatches 290; Indels 12; Gaps 2;

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DB 1729 CCGGCCCATGAGAGACGTCGCGGCACTACGATGGGCAAGGACGTCGCGGCGGCA 1788
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DB 1789 GTTCGGCCTGACGACACGTCGACGACGCGGAGC-----GGCGAGAGACTGGC 1839
QY 800 cgttaagatctcgcgaagaagtaagatgacaaaggcaatcatcattgagagatgctag 859
DB 1840 GTGCAAGACGATCGGAGGCGGAAGCTGGCGCGGAGGAGGACGTGAGACGTGCGGCG 1899
QY 860 agaagtaaaattcttgagagcgctatcagggcacaataatctcgtcaaatctatgagc 919
DB 1900 GGAGGTGAGATGATGACACCACTCTCCGGCCACCCAAACGTGGTGGGCTCCGCGGCGC 1959
QY 920 atgtgagatgagcctcaatgtctacatgtcatgtgaattatgaggaaggaattgct 979
DB 1960 GTACGAGAGACAAAGACGAGCGGTGACACCTGCTCATGTGAGACTGTGCGGCGGAGACTCTT 2019
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QY 1040 acagatttgagcgtgtagcctctctgcatcttcgaagggtgtagcatgtgaattgaa 1099
DB 2077 CGCCATCGTGCAGATCGTCACACCTCCCTCAGGCGGATGATGACCGGAGACATCAA 2136
QY 1100 gccagagaattctccttcccaaccagggatgaagaatgctcccatgaagtgttat 1159
DB 2137 GCCGAGAACTTCTCTGCTGCTCAGAGAGAGAGAGAGCGCCCTCAAGCCGACCACTT 2196
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DB 2197 CGGCTCTCTGCTCTCTCAAGGAGGCGGAGCTGCTCAGGAGCATGCTGCGGAGCGCT 2256
QY 1220 ttatgttccccagaggtttacacagatcatatagtagaagcagacattgtgagtat 1279
DB 2257 CTACATCGGCGCCCGAGGTGCTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2316
QY 1280 aggtgtcaataacgtacattctgctctgtgcagtcgagccattcgggacg 1330
DB 2317 CGGCGTCATGCTCTACATCTTCTCTCGCGGCGGCTGCTCCCTTGTGGGAGG 2367

RESULT 14
US-08-459-504B-26
Sequence 26, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nallini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlino, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttle, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6075185artle Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: May 2, 2002, 04:38:15 ; Search time 2003.89 Seconds

(without alignments)
12730.478 Million cell updates/sec

Title: US-09-854-731-3

Perfect score: 2374
Sequence: 1 gcacgaggcgatccgacat.....ccacatccccccctcagcg 2374

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estlin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: qb_estl:*
11: qb_estl2:*
12: qb_hic:*
13: qb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_huv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	522.8	22.0	851	10	AM448132 BRY_1726
2	478	20.1	597	10	AM257900 687063G05
3	454.4	19.1	562	11	BF422010 FMI_11.G0
4	386	16.3	491	10	BE590469 WHE0854.F
5	365.8	15.4	655	10	AM685958 NF032B03N
6	363	15.3	622	11	BF520876 EST458349
7	357.2	15.0	758	11	BG592840 EST491518
8	356.6	15.0	557	11	BG357062 OV2_9_D12
9	353.8	14.9	743	11	BG351862 135B07 Ma
10	337.2	14.2	491	11	T18715 5C04G11-T7
11	333.6	14.1	571	11	BF421980 FMI_11.G0
12	333.6	14.1	653	10	AT487355 EST245677

13	332	14.0	653	10	AT489424	EST247763
14	325.4	13.7	551	10	AM688043	AM688043 NF003F12S
15	321.8	13.6	326	10	AU032386	AU032386
16	321	13.5	644	11	BE942153	BE942153 EST421732
17	314.8	13.3	597	10	AV833696	AV833696 AV833696
18	311.2	13.1	382	11	T18633	T18633 5C07B02-L7
19	307.2	12.9	571	10	AT759795	AT759795 sb64d02.Y
20	302	12.7	602	10	AT774674	AT774674 EST355774
21	297.6	12.5	576	10	AT487605	AT487605 EST245927
22	295.4	12.4	460	10	AM930981	AM930981 EST356824
23	293.6	12.3	544	10	AT759787	AT759787 sb64c02.Y
24	292.2	12.3	357	10	AM324597	AM324597 707029B11
25	283.8	12.0	671	11	BG126719	BG126719 EST472265
26	282.4	11.9	669	11	BG126958	BG126958 EST472604
27	281.4	11.9	666	11	BG447969	BG447969 NF105A04E
28	280.8	11.8	532	11	BG790072	BG790072 sae62903.
29	280.4	11.8	707	11	BF292168	BF292168 WHE2207.E
30	272.6	11.5	474	10	BE056312	BE056312 945032H05
31	267.4	11.3	562	10	AT166280	AT166280 xylem.est
32	266	11.2	656	10	BE317046	BE317046 NF063B02L
33	266	11.2	659	11	BG456575	BG456575 NF082D02P
34	261.4	11.0	618	11	BF595411	BF595411 su65h04.Y
35	259.8	10.9	590	11	BI422962	BI422962 EST333628
36	257.8	10.9	680	11	BG586813	BG586813 EST488582
37	251.8	10.6	416	10	AV428222	AV428222 AV428222
38	251.2	10.6	498	10	AM030900	AM030900 EST274207
39	250.2	10.5	678	11	BI208239	BI208239 EST526279
40	242.4	10.2	640	10	AM033249	AM033249 EST276820
41	240.2	10.1	626	10	AM775106	AM775106 EST334257
42	235.6	9.9	702	10	AM565870	AM565870 LG1_352-G
43	235	9.9	423	11	C22392	C22392 C22392 Rice
44	233.2	9.8	599	11	BF638757	BF638757 NF064E02P
45	228.4	9.6	697	11	BG356745	BG356745 OV2_9_D12

ALIGNMENTS

RESULT 1
LOCUS AM448132 851 bp mRNA 03-JAN-2001
DEFINITION BRY_1726 BRY Trilicium aestivum cDNA clone p46-11G, mRNA sequence.
ACCESSION AM448132
VERSION AM448132.1 GI:12018793
KEYWORDS EST.
SOURCE Trilicium aestivum
ORGANISM bread wheat.
REFERENCE 1 (bases 1 to 851)
AUTHORS Clarke,B.C., Hobbs,M. and Appels,R.
TITLE Genes active in developing wheat endosperm
JOURNAL Unpublished (2000)
COMMENT Contact: Bryan Clarke
Division of Plant Industry
C.S.I.R.O.
GPO Box 1600, Canberra, ACT, Australia
Tel: 61 2 6246 5054
Fax: 61 2 6246 5000
Email: bryan@dpi.csiro.au.

FEATURES
source
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/organism="Trilicium aestivum"
/cultivar="WYuna"
/db_xref="taxon:4565"
/clone="P46-11G"
/clone_lib="BRY"
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BASE COUNT 233 a 172 c 193 g 250 t 3 others
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Db	487	GAGGAATAATTCGCGAACAACCTTTTCAGCACTTTGAACAAGAGGGCAACCGATTATATCA	546
QY	1911	gtcggaggaatgacacaggaattaaattctgtctcccaactcatctacat	1960
Db	547	GTTAGAGGATTAGCACAGGAACTAAATCTGGCGCCGACACATTACTTCAT	596
RESULT	3		
LOCUS	BF422010	562 bp	EST
DEFINITION	FM1_11.G09.b1.A003 Floral-Induced Meristem 1 (FM1) Sorghum		28-NOV-2000
ACCESSION	BF422010		
VERSION	BF422010.1		
KEYWORDS	EST.		
SOURCE	Sorghum propinquum.		
ORGANISM	Sorghum propinquum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC		
AUTHORS	clade; Panicoidae; Andropogoneae; Sorghum.		
	1 (bases 1 to 562)		
	Cordonnier-Pratt,M.-M., Gingle,A., Sudman,M., Marsala,C. and Pratt		
	,L.H.		
Title	An EST database from Sorghum: floral-induced meristems		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Cordonnier-Pratt MM		

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: empratt@uga.edu
Sequences have been trimmed to exclude POLYA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
Seq primer: JEN REV
High quality sequence stop: 556
POLYA-No.

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1.	562	Location/Qualifiers
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		/db_xref="taxon:132711"
		/clone_lib="Floral-Induced Meristem 1 (FMI)"
		/note="Organ: Floral-induced meristems; Vector: pBluescript II from Lambda Zap II; Site.1: XhoI; Site.2: EcoRI; mature plants were placed in a growth chamber for 15 days with 16 hr darkness and 8 hr light (flowering is induced by short-day conditions); 16 days after being returned to the greenhouse under natural long days during late April/early May, meristems were harvested. The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."
BASE COUNT	139 a	117 c 162 g 143 t 1 others
ORIGIN		

Query Match	19.1%	Score 454.4	DB 11	Length 562
Best Local Similarity	88.1%	Pred. No. 1.2e-63		
Matches 494; Conservative	0	Mismatches 67	Indels 0	Gaps 0

OY 620 cggcggcgctgtgagaggccgcgatctgggcgagagaagagccatctgacaaagactt 67
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Dd 2 CGGCGGGCCGTGCGGCTGTAATTCCGCCAGAGCCGAGCACCCTTGTCACAGACGTT 61

Dy 680 cgggtcttcgaagaacttcgcgcgaaagtacagatcgcggaagggttctgysgaagygcca 739
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Db 62 TGGCTTGGCCAAGACTTTGCGGCCAAGTCACGACTCCTGGGAAGAGGTCCGGAGGGGCCA 121

QY 740 cttcgacacacttgctccgcgtcgtcaagaagggcgagtacaagggacagaccgtcgc 799

Db	122	CTTTGGCCACACCTCTCTCCGCGCTGCACGAAGGGCGAGTACAAAGGGCCATATACCGTTG	181
QY	800	cgltcaagatcgcgcgaagaagctbaagatgacaacggaatccatltgagatglttcgtag	859
Db	182	CGTCAAGATCATCTCCAAAGCTAATGATGACAACGGCCATTTCCATTGGAAGATGTTCTG	241
QY	860	agaagtataaatlttgagaagcgltacagggacacatatctcgtccaattctatagatgc	919
Db	242	GGAAATCTAAGATTTTTTGAAGGCTCTATCAGGGGCACATATATCTCGTCAAAATTCCTAAGATGC	301
QY	920	atgttagagatgagcctcaatgltcaccatgtgtcaatgtgaaatagttagagagagaattgct	979
Db	302	ATGTAGAGGACGCCCTCAATATGCTTACATTTGTCTATGAAATTAATGTGAAGGTGGAGATTTGCT	361
QY	980	agacagaatatatagccaagagcgaggagatacacagaaggaagaatgtccaaacgcatgtgt	1039
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QY	1040	acagaatlttgagcgtagtagctctctcgtcacccttcgaagggatagtgcatcgtatltgaa	1099
Db	422	ACAGATTTTGAACGCTAGTAGGCGCTTCTGTGCATCTTACAGGAGATGATGCAATCGGATTTTGA	481
QY	1100	gccagaagaatltccctlttcacaaaccaaggagatgaaaatgctcccatgaagtltgattgattc	1159
Db	482	GCCAGAGAAATTTTCTTTTTCACAGACAGAGAGATGAMAGCGCTCTATGACAGTTGATTCGACTT	541
QY	1160	tgtctctcgtatctcaatag 1180	
Db	542	TGCTCTGTCTGATTTTATTTAG 562	

RESULT	4
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DEFINITION	WHE0854_F06.L1225 wheat 20-45 DAP spike cDNA library Trilicum
ACCESSION	aestivum cDNA clone WHE0854_F06.L12, mRNA sequence.
VERSION	BE590469
KEYWORDS	BE590469.1 GI:9845542
SOURCE	EST.
	bread wheat.

ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
<i>Triticum aestivum</i> Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidaeae ; Triticeae; Triticum.	Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsiao, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.	The structure and function of the expressed portion of the wheat genomes - 20-45 DAP spike cDNA library	Unpublished (2000)	Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: andersen@w.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with pired score less than 20
Seq primer: StrataGene SK primer.
Location/Qualifiers
I..491

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/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0854_F06_L12"
/clone_1b="wheat 20-45 DAP spike cDNA library"
/tissue_type="Spike and seed"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/notes="Vector: Lambda uni-ZAP XR, excised phagemid;"

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Site-1: Ecori; Site-2: XhoI. Plants were grown in the greenhouse. Spikes at 20 DAP and seeds at 30 to 45 DAP were harvested, total RNA and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give plasmid phagemids in the TJ Close Lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors).

BASE COUNT 131 a 107 c 119 g 133 t 1 others
ORIGIN

Query Match 16.3%; Score 386; DB 10; Length 491;
Best Local Similarity 86.6%; Pred. No. 1,2e-52;
Matches 425; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1664 accgctgttcaagcactgactcactcctgtgtcgagatgaacaaggcagatccgctg 1523
DB 1 ACACCTGTCCAGGCAATGACACCCCTTGGTTCGGGATGACCAAGACAGATTCGCTG 60
QY 1524 gacatcactcctcagatgaatgaacatcctcgcgtctacactcttaacgctg 1583
DB 61 GATTTCTTGTCTACATTAATTAAACATACCTTGTGCACTCTCTTAAAGCTTGG 120
QY 1584 gcatlaaaggcactacacaggcttlaaggagaatgaacttctatctcaactcag 1643
DB 121 GCGCTAAGGCAATTCACAGGCTTTAAGGATGATGACCTTGTATTTAGGCTACAG 180
QY 1644 tttaactgtctgacttgaagatgggtttgtatcacttacaacttgcgaagcacta 1703
DB 181 TTGATCTGTCTGAACATTAAGAGAGGAGTGTGTCACTTACAACTTCCGACGCTTTA 240
QY 1704 acgagatattaaactgtctatgaagaatcgaggttcttgaattttgcatgctg 1763
DB 241 ACGGGATATCTACTGATGATGAATGAAGATTCATGATTTTTCATGCTTGG 300
QY 1764 gaaccacttgcatacagaagaatgacttgaagagttctgtccgagcaatcactc 1823
DB 301 GAACCACTTTCATACAGAGATATGATTCGAAGAAATTCGTGCCGACGATTAAGCCCT 360
QY 1824 taccagcttgaaggcagcaggaagggtggagagatgtctgaaacagcttccagcaatt 1883
DB 361 TACCACTTCAGAGCCCTGGACAGATGGAGAAATGCTGGAACAGCTTTTTCACACTTT 420
QY 1884 gaacaaaggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1943
DB 421 GAACAGAGAGGCAACGAGATATATGATGAGAGAGTGGCAGACAGAACTAAATCTTGGCT 480
QY 1944 ccaactcatca 1954
DB 481 CCGACTCATTA 491

RESULT 5
LOCUS AM685958 655 bp mRNA EST 20-DEC-2000
DEFINITION NF032B08NRJ1000 Modulated root Medicago truncatula cDNA clone
ACCESSION AM685958
VERSION AM685958.2 GI:11931128
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 655)
REFERENCE Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
AUTHORS Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May
G.D. and Palva,N.L.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation

JOURNAL Medicago truncatula modulated root library
COMMENT Unpublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7560694.
CONTACT Palva NL
PLANT Plant Biology Division
INSTITUTION The Samuel Roberts Noble Foundation
ADDRESS 2510 Sam Noble Parkway, Ardmore, OK 73402, USA
TEL: 580 221 7317
FAX: 580 221 7380
EMAIL: nlpalva@noble.org
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PLATE Plate: 032 row: B column: 08
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1..655
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/clone_lib="Modulated root"
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/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Four-week old Rhizobium
meliloti-inoculated Medicago truncatula roots, containing
a mixture of young and old roots and nodules."

BASE COUNT 186 a 97 c 166 g 206 t
ORIGIN

Query Match 15.4%; Score 365.8; DB 10; Length 655;
Best Local Similarity 75.5%; Pred. No. 2e-49;
Matches 493; Conservative 0; Mismatches 157; Indels 3; Gaps 3;

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DB 2 TTGGTCATATCTTGTGGCTTAAGGAGAAAGTGAACCTTAAGGAATTTGATGACT 61
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DB 62 GTCAAATCATTTTCAACAGCTAAGATGATCTTCAAGCATTCAGATGAGAGAGA 121
QY 861 gaagtaaaaatttggagagcgtatcaaggacacataatctgcgaattctgatgca 920
DB 122 GAGGTGAAAATGTGTAAGGCTTATCTGCAATAGGAATTTGGTCAAGTTTATGATGCA 181
QY 921 tctgagagatgacctcaatgtctcatctgcatctgcaatctgtgaaggagagatgcta 980
DB 182 TTGAGAGATGTGAATTAACGCTTCAATTTGATGAGATGTGCGAGGTGAGATTAAG 241
QY 981 gacagaaatlagccagagcgaggagatatacacagaggaagatgccaaacgcatgtgta 1040
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QY 1041 cagatttgaagcgtatgactctctgtcatctcagggggtagtgcatcgtgattggaag 1100
DB 302 CAATTTCTGAATGTAGTTCCTTTTGTCAATCTCCAGGAGAGTGTTCATGCGCATTAAGA 361
QY 1101 ccagaaatttcccttcccaacacagaggaatgaatgctcccaatgaagtgtgatttt 1160
DB 362 CCAGAAATTTTCTTTTGTGTCACAAAGATGAGAGATGCTGTTGAAATTTATGATTTT 421
QY 1161 ggtctctgatttcaatgaccagatgaaggcttaatgatatgttgaagtgtcatat 1220
DB 422 GGTCTATCTGATTTTGTAGACACAGCGCGCTCAATGATATTTGTTGTTGCTAC 481
QY 1221 tatgttgcacagagaggttttaacagatcatatagatgtgaagcagacattggaagata 1280
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QY 1281 ggtgtcaacgttaacttctgctgtgagcagtgagcc-attctgggacagaaagaat 1338
DB 542 GGAGTTATATCTTACATATTTGTTATGTGGAAGTGAACCGCTTTTGGGACGACAGAA 601
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OY	1291	cgtacat	1297
DB	549	CTTATAT	555
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LOCUS	BG351862		
DEFINITION	135B07 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA sequence.		
ACCESSION	BG351862		
VERSION	BG351862.1		
KEYWORDS	EST.		
SOURCE	potato.		
ORGANISM	Solanum tuberosum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.		
AUTHORS	Nielsen,K.L., Crookshanks,M., Emmersen,J. and Welinder,K.G.		
TITLE	EST-sequencing of mature potato tuber (Var. Kuras)		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Karen G. Welinder Institut for Biotechnologi Aalborg Universitet Sohngaardsholmsvej 49, 9000 Aalborg, Denmark Tel: +45 96358467 Fax: +45 98141808 Email: kgye@bio.auc.dk Sequenced from the 5' end. High quality sequence stop: 743 POLYA-No.		
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Matches	500; Conservative 0; Mismatches 222; Indels 3; Gaps 1;		
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DB	6	TATAATAGCATGGAGATTATGTAAAGAGAGAGAAATGTGCGACCGATACTTCACAAGGGCT	65
OY	1002	gggagatcacacagagaaagatgccaaaagcgattgtgttcacagaattttgaagctagtagcc	1061
DB	66	GGAAGAATFACTCGGAGAGACGATGCCAAAGCTGCATGTCGCAACTTTAAGCTGTGCTCG	125
OY	1062	tctcgtcatcctcaaggggtagtgatcgatcggtgatcttgaagccagagaatttcctttcaca	1121
DB	126	TACTGTCAATCTTCAGAGGGGTTGTGTATGCGCGACCTAAAGCCTGAAGAAATTTCCCTTTCGT	185
OY	1122	accagagatgaaatagctcccacatgaagttaattgatttgtctctccttgatttcattaga	1181
DB	186	TCTTAAGGATGAACCTCTCTCTTTAAAGGCCATGTGACTTTGGCTTTCGATTATGTAANA	245
OY	1182	ccagatgaaggcttaatgatalctgttgaagtgatatactatgttccccagagaagtlta	1241
DB	246	CCAGATGGAAGGCTTAATGATATTGTGCGAAGTGCACTACTATGTTGCACCCTGAGGTTTG	305
OY	1242	cacagatcataagcatatggaagcaaacatttgaagtatagtggtcataacgttaactctg	1301
DB	306	CATGATCTTATGGAACGAAGCTCACATGTGAGGATATTGTGTAATTCATATATTTCTT	365

QY	1302	ctctgtgcagtcgcccattctggcaacgaatcaggaatatccagatctgltg	1361
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QY	1362	agagctgatacccaactttgatagtatccagctggtcctacagatcagctgaagctaaagat	1421
Db	426	AAACGTATCCAAACCTTGGACGAATCCCTTGGCCCTCTTGTCTGTGATGCAGTAAAC	485
QY	1422	tttgttgaaaggaattcttgaaacaaagattaccgcaaaagaatgaacgcgtgttctaagcat	1481
Db	486	TTTTGTAAAAAGATTGCTGTAATAGGATTTATCGAAAAAGGCTATACGTGACACTGAGCTTC	545
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Db	546	AGTATCTCTTGTTGGCTGGCTGCATTCATGCAGTGAAGATTTCTTTGGATATGATTAATAT	605
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Db	666	GCTTAAGCAATTGGCTATATACCAACAATAGCTTATCTCTGTATCAGTATTAACACTATTAGG	725
QY	1659	cttag 1663	
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LOCUS	DEFINITION	RESULT 10
T18715	5C04G11-7' membrane-free polysomes from endosperm Zea mays cDNA clone 5C04G11 5' end similar to calcium dependent protein kinase.	17-OCT-1996
T18715	491 bp mRNA	EST
T18715	mRNA sequence.	

ACCESSION	T18715	GI:485645
VERSION	T18715.1	
KEYWORDS	EST.	
SOURCE	Zea mays.	
ORGANISM	Zea mays	

REFERENCE
AUTHORS

Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida, Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 491)

Shen, B., Canello, N., Torres-Jerez, I., Stevenson, R., McCreery, T.,

TITLE	Partial sequencing and mapping of clones from two maize cDNA libraries
JOURNAL	Plant Mol. Biol. 26, 1085-1101 (1994)
MEDLINE	95111093
COMMENT	Contact: The Maize cDNA Project

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Rob Ferl
Interdisciplinary Center for Biotechnology Research
DNA Sequencing Core
University of Florida

QY	2118	catatgagaccatgatgatgatttccctccctcgtctctatacct--ctggaataatg	2175
Db	414	-ATTATATGAGCCCGCATTTGCTTTATACCCCTGCTCTCTCTGCGCCCTTCCTTTGG	472
QY	2176	atcattatctgttcgctgcctcgcgtgttcatacatagattttgtagaata	2235
Db	473	TCAATGACCATTCCTGTTTGATGATGATCGCCGCTTGTGTCTGCAATAGCTTTGTAGACTA	532
QY	2236	catgtaagaatcttt	2251
Db	533	CATGTAAGATCCTCT	548
RESULT	12		
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DEFINITION	EST245677	tomato ovary, TMU	Lycopersicon esculentum cDNA clone
ACCESSION	U01487355		mRNA sequence.
VERSION	U01487355.1	GI:4382726	
KEYWORDS	EST.		
SOURCE	tomato.		
ORGANISM	Lycopersicon esculentum		
REFERENCE	Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;		
AUTHORS	Lycopersicon.		
1	(bases 1 to 653)		
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Romling,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nieman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksey,S.D. and Giovannoni,J.			
Generation of ESTs from tomato carpel tissue			
Unpublished (1999)			
TITLE	Journal		
COMMENT	Contact: CUGI		
	Clemson University Genomics Institute		
	Clemson University		
	100 Jordan Hall, Clemson, SC 29634, USA		
	Email: http://www.genome.clemson.edu/orders/index.html .		
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	/lab_host="XLI-Blue MRP"		
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ORIGIN	193 t		
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Best Local Similarity	69.5%;	Pred. No. 2.9e-44;	
Matches 453; Conservative	0;	Mismatches 199;	Indels 0; Gaps 0;
QY	1366	ctgaccccaacttgatgattaccggtgtgctcaagatcatgactgaagctaagatttg	1425
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QY	1426	tgaatgatttcctggaacaagaatcccgcaaaagaatgacgcgtgttcaagacgactc	1485
Db	61	TGAAAAGCGTTTGTGATTAAGACCATAGGAAGAAGATGACTCTTCTCAAGCAGTCGACTC	120
QY	1486	atcctgtgttcgagatgaaacaagaagcgactccgctgagacatactcatcagattaa	1545

FEATURES	source
LOCUS	AI1489424
DEFINITION	AI1489424 653 bp mRNA EST 18-MAY-2001
ACCESSION	EST247763 tomato ovary, TMU Lycopersicon esculentum cDNA clone
VERSION	AI1489424
KEYWORDS	AI1489424.1 GI:4384795
SOURCE	tomato.
ORGANISM	Lycopersicon esculentum
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
AUTHORS	Lycopersicon.
TITLE	1 (bases 1 to 653)
JOURNAL	Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
COMMENT	,C.L., Niernan,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley ,S.D. and Giovannoni,J. Generation of ESTs from tomato carpel tissue Unpublished (1999) Contact: CUGI Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Email: http://www.genome.clemson.edu/orders/index.html . location/Qualifiers
FEATURES	1..653
source	/organism="Lycopersicon esculentum" /cultivar="TM96" /db_xref="taxon:4081" /clone="cLED1A12" /clone_1b="tomato ovary, TMU" /tissue_type="carpel" /dev_stage="5 days pre-anthesis to 5 days post-anthesis" /lab_host="XLI-Blue MR" /note="Vector: pBluescript SK(-), Site_1: EcoRI; Site_2: XhoI; cLED - Tomato Carpel EST Library. OligodT-primed and

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DEFINITION	AU032386	Rice root	Oryza sativa	CDNA clone	R3979_1A,	mRNA sequence	
ACCESSION	AU032386						
VERSION	AU032386.1	GI:3768359					
KEYWORDS	EST.						
SOURCE	Oryza sativa.						
ORGANISM	Oryza sativa.						
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.						
AUTHORS	1 (bases 1 to 326)						
TITLE	Minobe, Y. and Sasaki, T.						
JOURNAL	Rice CDNA from root						
COMMENT	Unpublished (1995)						
	Contact: Takuji Sasaki						
	National Institute of Agrobiological Resources						
	Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki						
	305-8602, Japan						
	Tel: 81-298-38-7441						
	Fax: 81-298-38-7468						
	Email: tassaki@agr.affrc.go.jp, URL: http://rpg.dna.affrc.go.jp/PROJECT="RGP"						
FEATURES	Location/Qualifiers						
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ORIGIN							
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Best Local Similarity	99.1%; Pred. No. 2,7e+42;						
Matches	323; Conservative 0; Mismatches 3; Indels 0; Gaps 0;						
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OY	1326 gacagcaacgaatcgggaatatccgactctgtgttgagagcgcgattcccaacttgatgat						
DB	61 GCACCAACAGAAATCGAGATATTCGATCTGTTGAGAGCGATCCCAACTTTGATGAT						
OY	1386 tcaacgtgtgctcacaagatcacaagctaaaggaatttggtaagaagattcttgaacaaa						
DB	121 TCACGTGGCTTCACGATATCAGCTGACGTAAAGATTTTGTAAAGAGATTTCTGAACAAA						
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DB	181 GATTACCGCAAAAGATGACCGCTGTTCAAGCAGCATCATCTTGTTGGAGATGA						
OY	1506 caaagcgagatccgcctgagacatactcatcttcagatlaattaagaacatacctcgcgct						
DB	241 CAAAGCGAGATCCCGCTGACATCTTCAGATTAATTAAGCAATACCTCCGCGCT						
OY	1566 aacactttaacggttgacataa 1591						
DB	301 ACACCTTTAAAGGATTCGATTA 326						

Search completed: May 2, 2002, 06:25:09
Job time: 6414 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2002, 06:30:06 ; Search time 80.44 Seconds
(without alignments)
573.690 Million cell updates/sec

Title: US-09-854-731-4

Perfect score: 3260
Sequence: 1 MGCCYKGASGRADDEGV.....LGFTKLHGVTIRCSNTRRH 623

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1970	60.4	594	21	Arabidopsis thaliana
2	1948.5	59.8	594	21	Arabidopsis thaliana
3	1801.5	55.3	502	21	Arabidopsis thaliana
4	1790	54.9	504	21	Arabidopsis thaliana
5	1596	49.0	428	21	Arabidopsis thaliana
6	1534	47.1	414	21	Arabidopsis thaliana
7	1377	42.2	368	21	Arabidopsis thaliana
8	1065.5	32.7	523	21	Arabidopsis thaliana
9	967	29.7	426	21	Arabidopsis thaliana
10	934	28.7	265	21	Arabidopsis thaliana
11	908.5	27.9	463	21	Arabidopsis thaliana

12	903.5	27.7	529	21	AA629590
13	903.5	27.7	542	21	AA629589
14	868.5	26.6	459	21	AA629591
15	855.5	26.2	856	21	AA638599
16	855.5	26.2	893	21	AA638598
17	855.5	26.2	1017	21	AA638597
18	852.5	26.2	538	21	AA643621
19	847	26.0	384	21	AA610103
20	824.5	25.3	501	21	AA635776
21	816.5	25.0	483	21	AA631158
22	816.5	25.0	556	21	AA631157
23	808	24.8	512	20	AA693256
24	788	24.2	404	21	AA646566
25	764	23.4	226	21	AA648299
26	748	22.9	378	21	AA646567
27	747	22.9	569	15	AA656237
28	743	22.8	425	21	AA635777
29	723	22.2	408	21	AA631159
30	703	21.6	424	21	AA643622
31	700	21.5	399	21	AA635778
32	699	21.4	421	21	AA643623
33	697	21.4	274	19	AA649837
34	548	16.8	456	16	AA674996
35	538	16.5	524	21	AA618304
36	524.5	16.1	307	20	AA693255
37	512.5	15.7	355	22	AA650055
38	512	15.7	356	22	AA684360
39	510	15.6	517	18	AA630919
40	509.5	15.6	355	22	AA641268
41	509.5	15.6	357	22	AA603508
42	507.5	15.6	385	22	AA639482
43	507.5	15.6	385	22	AA684359
44	503	15.4	502	21	AA654580
45	500	15.3	389	21	AA68793

ALIGNMENTS

RESULT 1

AA653883
ID AA653883 standard; Protein; 594 AA.

AC AA653883;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 68643.

KW Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PE 25-FEB-2000; 2000EP-0301439.

PF 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0127462.

PR 01-APR-1999; 99US-0128234.

PR 06-APR-1999; 99US-0128714.

PR 08-APR-1999; 99US-0129845.

PR 16-APR-1999; 99US-0130077.

PR 19-APR-1999; 99US-0130449.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
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PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
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PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
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PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
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PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
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QY	476 ELVYLKLOFLKLEPRDGVSLDNFRTALTRYLTDAKESRYLEFHALEPLAYARRMDEE	535			
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DB	414 fcaasvsvyqIleaIeeweqIatvafefesegsraIsvqelaemsIpnaypIldkwlr	473			
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XX	Protein identification: signal transduction pathway; metabolic pathway;				
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QY 234	NNLVKDYACBDGLNVYIVMEICEGEGELDLRLAKGRGTEDAKAIYQIUSVAFCL	293		
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QY 474	EDELLYLKDLKLEPRRGVFSLDNFRALRYTLDAKESKRVLEFLALDEPLATRRDF	533		
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DT 17-OCT-2000 (first entry)
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XX Protein identification; signal transduction pathway; metabolic pathway;
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KW termination sequence.
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PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145921.
PR 02-AUG-1999; 99US-0146386.
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PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
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PR 10-AUG-1999; 99US-0148171.

PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148365.
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PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 23-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149920.
PR 25-AUG-1999; 99US-0150366.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155559.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
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PR 13-OCT-1999; 99US-0159293.
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PR 14-OCT-1999; 99US-0159329.
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PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match

49.0%; Score 1596; DB 21; Length 428;

Best Local Similarity 70.1%; Pred. No. 1,3e-116;

Matches 298; Conservative 68; Mismatches 59; Indels 0; Gaps 0;

Oy 197 KGTVAVKIITAKAKMTAISIEDVREVKIIRALSHNNLVKFTDACEDEGLNYITVMEIC 256
Db 2 kngtvavkiiskamtslistsedvrevkiklksjrhmvkfydyedadvitvmeic 61

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PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
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PR 18-AUG-1999; 99US-0149426.
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PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
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PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
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PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 22-OCT-1999; 99US-0160980.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 47.1%; Score 1534; DB 21; Length 414;
Best Local Similarity 69.6%; Pred. No. 9, 1e-112;
Matches 286; Conservative 64; Mismatches 61; Indels 0; Gaps 0;

OY 211 MTTAISTEDVREVKILRALSGHNNLVKFPYDACEDEGLNVTYVMELCBGGELDRILARG 270
DB 1 mtsalsiedvrevkllkalsghnmvkvfydvfedsdnfvvmelceggelldsllarg 60
OY 271 RYTEDAKAIYVQILSVAFCHLOGVYHRODKPENLFTTRDENAPMKLIDFGISDFIRP 330
DB 61 tyeaaekrlllvqllsatatfhlqgvvnrldkpenflitsknedavlkvidfglsdyarf 120
OY 331 DERINDIGSAYVAPEVLRHSYSEADWISIGVITYTLLCGSPFPMARTESGIFRSYL 390
DB 121 dqrindvgsayvapevlnhsysteadwisyllcgspifgtrtsaalfrcylr 180
OY 391 ADPNFDDSPWPTVSAEAKDFVKRLNKDYRRMRAWQALTRPWLDEORQIPLDILFRL 450
DB 181 anpfdldpwpstpsiafdvfkrlnkdkrmtaagalahpwlrdenpgyllldfslykl 240
OY 451 IKOYLRAPELRLKALKASKALREDELIXLKQFKLEPRRGFSLDNFRALTRYLDA 510
DB 241 vksyiraspftraalkskskaipееelvfllkaqimllpepdgqllhlnftalltryadca 300
OY 511 MKESRVLEFLHALPLAVRRMDPEFCNAATSPYOLEALERMEEIAGTAFOOFEOGNRV 570
DB 301 miesrlpdlmmgplakkkldfееfcaasvvyglaeeeweglatvafefeesgira 360
OY 571 ISVEELAOELNLAPTHRSIVQDWIRKSDGLNFGFTKFLHGVTIRGSNTR 621
DB 361 isvgeleaeemslgnpnaypllkdwlrtsldgkinflgyakflhgvtvrsssr 411
RESULT 7
AAG48297
ID AAG48297 standard; Protein: 368 AA.
XX
AC AAG48297;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60975.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
PD
XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 09-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132865.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134219.
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PR 21-MAY-1999; 99US-0135124.
PR 24-MAY-1999; 99US-0135353.
PR 25-MAY-1999; 99US-0135629.
PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136392.
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PR 10-JUN-1999; 99US-0138647.
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PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139819.
PR 23-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 24-JUN-1999; 99US-0140354.
PR 28-JUN-1999; 99US-0140695.
PR 29-JUN-1999; 99US-0140823.
PR 30-JUN-1999; 99US-0140991.
PR 01-JUL-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141642.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142303.
PR 09-JUL-1999; 99US-0142803.
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PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.

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PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145085.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 26-JUL-1999; 99US-0145224.
PR 27-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
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PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
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PR 13-AUG-1999; 99US-0148585.
PR 16-AUG-1999; 99US-0148684.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
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PR 23-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
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PR 08-OCT-1999; 99US-0158232.
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 PR 29-OCT-1999; 99US-0162142.

Query Match 42.28; Score 1377; DB 21; Length 368;
 Best Local Similarity 69.7%; Pred. No. 1.5e-99;
 Matches 255; Conservative 59; Mismatches 52; Indels 0; Gaps 0;

QY 256 CEGSELDRIARGRYHEEAKAIWQIISVAFCHIQGVYHNDKRENFPTTRDNA 315
 1 ceggellidrlilargrypevdakrllyqlisatalfhlgvvhndlkpenlffsmeda 60
 316 PMKLIDFGLSDFRPDERLDIVGSAYVAPEVLRHSYSMDIWSIGVITYILCGSRP 375
 61 llkvldfglsdfrtydqlndvgsayvapevhlrsysteadmslgyisylilcgssrp 120
 QY 376 FWARTESGIFRSVLRADPNEDSPWPYVSADAKDFVKRFELKNDYRKMTAVQALTHPWL 435
 121 fgyrtesaifrcvrlraupnfedmpwpslprakdfvkrllkdhnrkmtaqaalahpwl 180
 QY 436 DEQROIPDLIIFRLIKOYLKATPLKRLAKLSKALREDELLYKLOFKLEPRDGFVS 495
 181 denpgllldfsvkyrvksyrlasprtsalalkalskarpdeevlflkaqfmlldpkdgls 240
 QY 496 LDNFRTALRVLTPAMKESRYLEFLHALEPLAYRRMDFEECAAIISPYQLEALRMEEI 555
 241 lncftmatrlatratdamessrlpdlintmqiaqkldfeetcaavsvyqleaaleweqi 300
 QY 556 AGTAFQEQEGCGNRVISEVLELAQELINAPTHYSIVQDMIRKSDGKLNFLGFTKFLHGYTI 615
 301 atsaftehebcnrlisvqelagemsygsaypilkdwirssdglstfgyakflhgytv 360
 QY 616 RGSNTR 621
 361 rrsasr 366

XX Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 OS Arabidopsis thaliana.
 XX EP1033405-A2.
 PD 06-SEP-2000.
 XX 25-FEB-2000; 2000EP-0301439.
 PF 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 23-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
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 KM Protein identification; signal transduction pathway; metabolic pathway;
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 KM termination sequence.
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QY	571	ISVEELAEELNLPRTNYSIVQDWIKRS-----DGKLNLFGLTTPKL	610								
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KW	hybridisation assay; genetic mapping; gene expression control; promoter;										
XX	termination sequence.										
OS	Arabidopsis thaliana.										
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Query Match 26.68; Score 868.5; DB 21; Length 459;
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QY 529 RRMDFEEPCAAISPYQLALERMEIAGTARQOFQDEBNRIVISVELAOLINLAPTHYS 588
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RESULT 15
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 AC AAG38599;
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 DT 18-OCT-2000 (first entry)
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 KW Protein identification; signal transduction pathway; metabolic pathway;
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termination sequence.
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OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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Query Match 26.2%; Score 855.5; DB 21; Length 856;
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Db 296 kgkvpreeskqevpreeskrevvngpesakpetkskpettkpettselkpetkaepq 355
QY 108 PRSPAHKIKATLTKAKRLGGKPRKEGTIREBGVAGGGGGAADAEATERPLDXTFGFSKN 167
Db 356 P-----khmriv-----ssaglrtesvlgfk---ten 379
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Db 380 kfefyglgkklgqgqfg-llfclckg--tneyackskskrltldedvedvireldim 436
QY 228 RALSGHNNLVKFEYDACEDELNVYIVMELCEGGLDRIILARGRYTEEDAKAIVQILSV 287
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QY 288 VAFCHLQGVVHNDLKRENLFTTRDENAPKULIDFGLSDFIRPDERLNDIVGSAYYVAPE 347
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